

Figure 1

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Figure 2

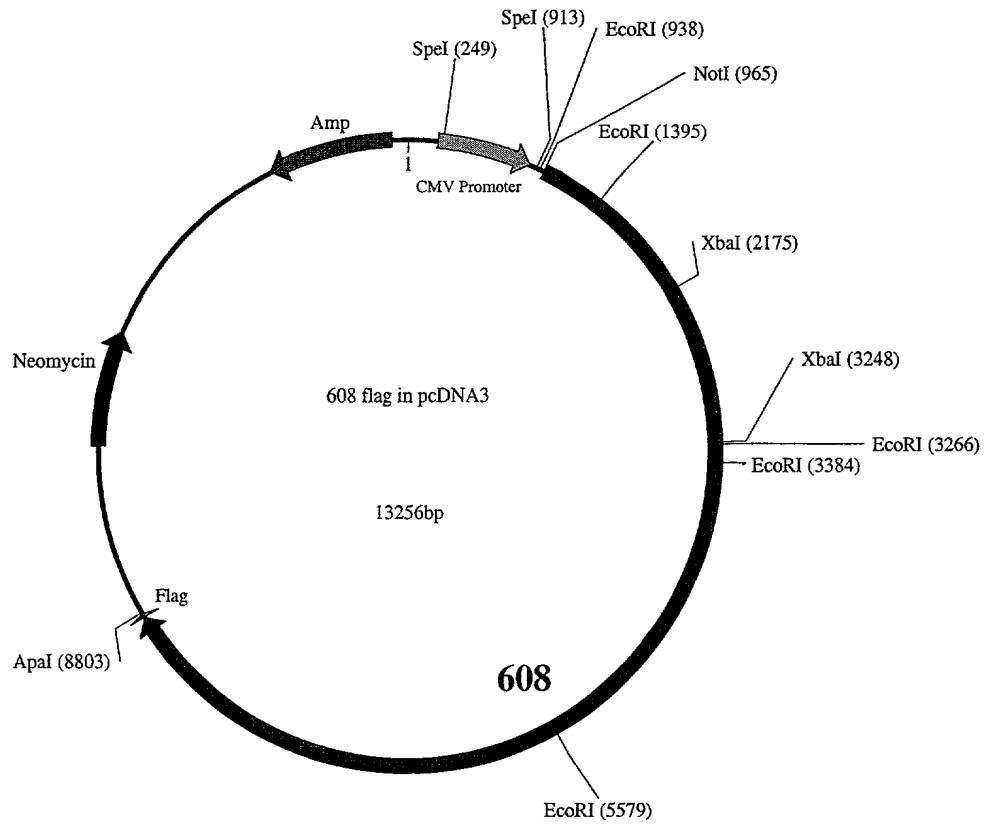


Figure 3

MQVRGREVSGLLISLTA VCLVVT PGSRACPRRCACYVPTEVHCTFRYLTSIPDGIPANVE
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Figure 4

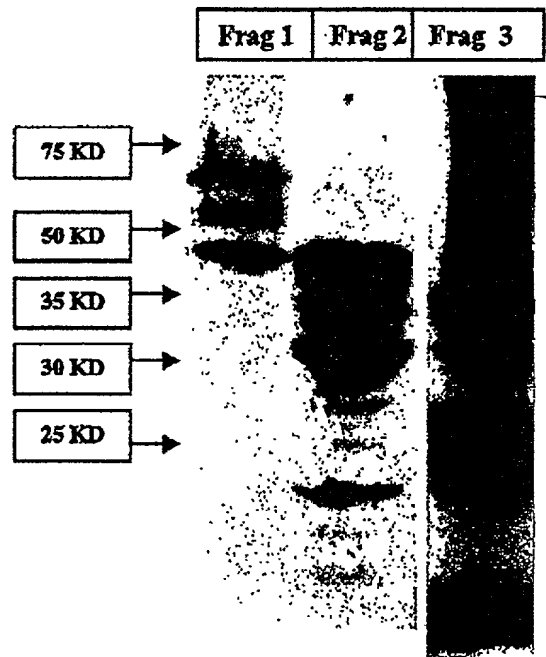


Figure 5

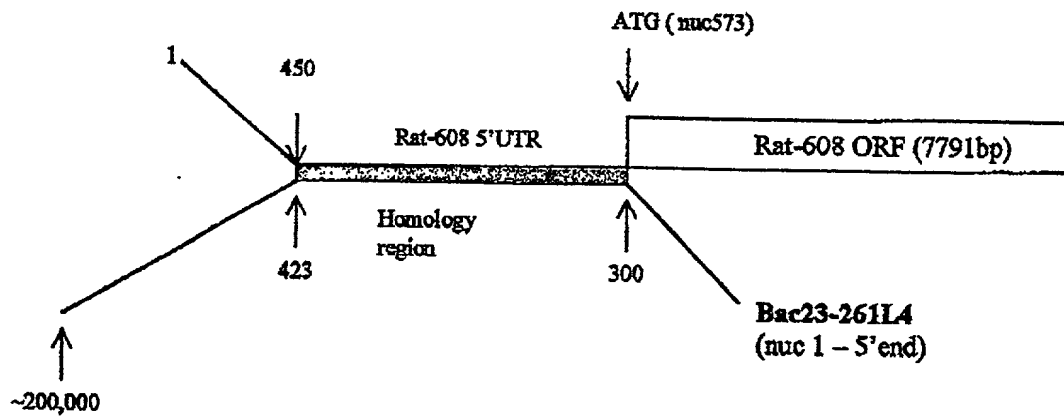


Figure 6

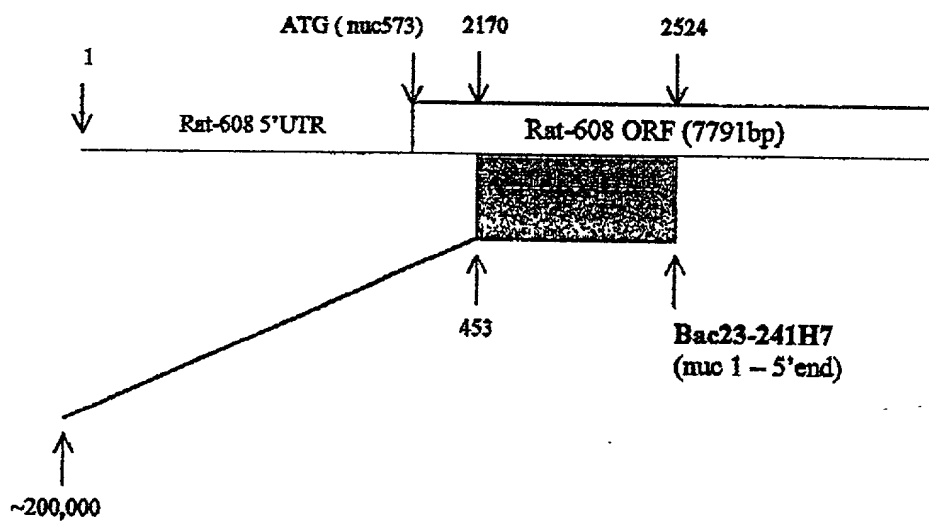


Figure 7

Nuc 1

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 TTTGGAACCAACCCAGATGCCCTCAACAGAGAAATGGGCCAGAAATGTGGTCCATTTA
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 GNATGGTCTGNAGGATCTTGAGTGAGGTAACCCAATCACAAAAGAACACTCATGGTATGC
 ACTCACTGATAAGTGGCTATTTGTCTATGGAGTGATTAAAAAGGGAAGAAGACACATAGC
 TTTTGTGTGTATAATATTAAGATGGAAATTTGCCAGTGCTGTTGGCTTATGAGTGAATCT
 TGTTTCAGTGGATTACCGGAAGAAAATAATAAGTGAAGTGTAGGAAGAAGTAGTTAATCA

Nuc 390

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Nuc 2317

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▼ Exon 1 (Nuc 3661)

★ Nuc 4203

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GCCATAAAAGATGAAATGCATAGCAATATGCAGAAATGGATGTCAACTGGAAATCAATTTG
GGCTAATCAAAAACAAGACAGACTCAAAAAGGAAACACCGTGTAGCTTCTCTGACAAACA
GAAGCTAGATTACACTTGTACGTGCGCATGTGTGTTAGAATTTTATTAGTTATACACT
ATTCTAATCTGTGAGTGTGTATAAAGGCATGCATGTAAAGCAAAAAACAAGCTAGCTGGGG
TGGTGTAGGAGAGAAAGCAATGAGAGGAGTTAATAAGAACGAAGCATAGTAACATAGGTG
CCAGGATGAAATGCATTAATTTGTATGCTAACTAAACCACAGACAGGAGGCCACAGTTCA
AACCAGGGTGAAATCCCAACACAGAGAAGGGGAAGTAGACACAAAGTTTCGCCACATAAC
CAAGAAGCCATTTCAGATTGCTGCCTGCTGGGAGGGGGCTCCAGTTTCTCCAGTCTGAC
ACTGTGTATAACAACCAAGTTGACAATACAAAGTTGGCATGATGGATGTTTTTGTGCTATT
TTTCATTTTCTTCTTACAGTTTGTGTGTGTGGTGGTGTGTGTGGTGGTGGCTGTGGTTTC
ATTGTTTCTTTTGAGAGAGAGAAGGAACATGAAATTGGGTGGGTAGGAAGCTGGAAAGC
ATCTGGAAGAAAGTTGGGGAGAGAGAAATTTGTATGGAGCATTTTAAACAAACAAACA
ACCAAAACAAAAGGTTTCATTTGCCACAAAAGGTTGTAATTAATTAACCAAGTTACGACT
CTTAAAGAAAATATTCCCAATTATTCCACAGAGTTGCTATGTATGCTGTGCCTAGGACTTTTG

▼ Exon 2 (Nuc 6559)

CTTGAACCTGGCCCTATAACTCTGGTGTGGTGTCTTTTCAGGATGCAAGAGAGGGCAGGGAA
 GTCAGCTGCTTGCTGATCTCCCTCACTGCCATCTGCCCTGGTGGTCACCCCTGGGAGCAGGGTC
 TGTCTCGCGGATGTGCCTGCTATGTGCCACAGAGGTGCACGTACATTTGGGAACCTGAAC
 TCCATCCCAGACGGGCATCCCAGCCAATGTGGAACGAGTCAATTTAGGGTGTGT

↑ Nuc 6755

GGACCTTGCTGATCTCCTTCTCAGAGAGGGGACCACTGATTTTCCTGGTACTTTGCCCCC
 AAACAACCTGTGATTACTTTTAATAGTTTCTTCTAAATGGGTTCATACAAACCTTATATTG
 TGGAGACAATGAACATTTTATCCCAATAGTCTTTTACTAGAAGTTGAAGCCCCTCTTAGTT
 GTTTGGGAGCCTCATAATTATGGGGCAGCTTTATTCTGAATGAATTTTAAATGAAAAAGAT
 ACAGTTTCTGTAAACAATCATTATGATACCAAGGAAGAGGAATTGTCAATTGAATATTTTAA
 AAAAGCATTTCTTTTGCAATTTATAAATACCCATTACAAAATGGCTTACTTAAAATACTTG
 CCTTACTAAATCTGACAAATTATGGTGATATTTGAAGGTTTATGAAAAATTGTTTATGTGT
 ATAAATGCACAAGAAATGGGATATGCCATCACCTATGTGCCATTAGTGAGCATGTACAGT
 ATGCCAAAACACTATTGTTTACCGTTTGGAGGAAGTAATGGGGTGGGGGAGCAACAAGGGT
 TATAACCGTATACCCAGTGCCCTTGAAGCGATTGCAAAACAGTAAAGACTGACATTGTGTT
 CTCCCTATGAGGGAGGGGCTTGGGCTGAGCATTGTGAATGAGCATTGTCTCATTGTCT
 GGCAGGTTTATGATAACTTGACCAAGCTAGAGTCACTGGAGAGGAAGGAACCTCAACT
 GAGAACATGCCTGAAGAAGATCAGATTATAGGCAGGCTGTGGGGCATTTCCTTAATTAG
 TGATTCATGGGGCAGGGCCAGTCCATTGTTCGTGGTACCATTTCACGGCACTATTAAAA
 AAAAAAACAAGGCTGAGCAAGTGTCAAGGAGCAAGTCAAGTGAAGCAGCAGCCCTAATGA
 TCTCTGCATCAGCTCCTGCCTCCAGGTTCTACCTTATTGAGTTCTGTCTAGCTCCCTA
 CAGTGATGAACAATGATGTGGAAGTATAAGCCAAATAAATCCTTTCTTCCCAACTTGCTG
 TTGGTCATGATGTTTCATCACAGTGATAATAGTCCTCATGAAGATGCTGGTGTATAACA
 CCTTTGGACTAAATCTGTATCTATAGCTGAGGAAAAATGGAGCATAGAAAGTCTCCAGA
 CTACACCAGAGTGAATCTGGGCTGAGCTTAGAATCACACCCACGTGCACTCCACTGCC
 GGGGCTTCTTAACCGGAACACAGTTGTAAAAAGGGAATTTCTGTTTGTTCCTTTTGACA

Exon 3 (Nuc 8089) ▼

TGTGGACTTTAATTGACGATTCTCTGAAGCTGAAAATGATTTTTCAGGTATAACAGC
 CTCCTAGATTGACAGAAAATGACTTTTCTGGCCTGAGCAGACTGGAGTTACTCATGCTGCACA
 GCAATGGCATTACAGAGTCAGTGACAAGACCTTCTCGGGCTTGCACTCTTGACAG

Nuc 8218 ▲

GTGAGATAGGTAGAGGGTGTGAGGGCTGAGAAGAGAGGTGCAACTGTGGGTATATACC
 AAAAGCTGCTGATTCCCGTGGGAGACATTCTATAAGCATTCTATAAACTAGAGGCAGATA
 TCAAGGAAGGATTCAATTGTAATGCAATTTTATGAGAAAATTTGAATATTAAGAAAATG
 CTGGGGAATAATGCTTACACAATTGCGAGGACCTAATTTAGGATCTCCAATAGCCACATAA
 AAAGCACAGCATGGCGGCAGACACCTGCAATTCCTGTCCCTGGAAGCACCTGTTTCAAGT
 CCCAGAGACTCATTTGGCCCAACACTCTATTCAATCAATGAAGTCCATATTCAGTGACAAA
 ACTTGACTCAGAAAATAATGTGGAAGCATCAGGAAGACAGCCAACATCTGGTCTTACT
 CATGCTATGAATAAGGATCCAGAGAGAAGGGAAGAAAAGGAAGGAAGGAAGGAAGG
 AAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGG
 AAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGG
 GGAGAAAAGAAGAGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGG
 TTTTATCCATAAAAGGTCATTTCCACCTGTTTGTCTGGAAGTAGAGTGGGATCCCTTATAT
 AAGGGCAGTCTTTAACAATAGTAGCATTTTATAAACCATTACAAATTTTGAGTTTCTCTAC
 TTTTATCTCTACCATCTTCAAACCTGAAACTACAATTATCCACAAAATGAAGAAAATGC
 TGTAAGAGTTTTCACACACCGAAGTGGGAACTTAAGGATTAGACAAGTCTAACAATGAG
 AATGGGGAGAACAAAAGAGACTGCACAGGGAGCCCTTTCTCTGCTTATAATCTTGACAC
 TTGAGAAGCTAATTGACGCTGCATGACTACTCAACTCTTTAAGCAAAACAATGCTGTTGTT
 ATGAAAAGGCACAAATAAAGTACATATGTCCATAATATTATCAAAATTTGCATGCAGCAC
 ATAATAGCAATCAAAGCAATAACACCCACTGTTTACAGAGACTTTAAACATGAAACTGGA
 ACTATGTCTAGTGTGTTGACTTAGGGTACATAGTATGCTGTGTCTGTATGTACCAATGTTG
 ATTTAGGTCATCAGACAGCATTGGAACATGTATCTTCAGGAGGAATCATTATGTATCT
 GCATGAAATTTCTCCACCTATGTTTATTCTCTTAGCCAGGTTTTCTCTGATGGAGAAACATT
 GGGTTTGAGGTTTACTCCAGGTAACATTAGGGAAAAGCTGTCTATGTTCTCAGTTTGG
 CTTTATTTATGAGGGATGTTGGTATTCCAGAAAATTCTCTTTGAAGAGATTACAATTTA
 GGTCAAAAACAGAAAAATATGTAAAAAGTTATTGTTTTATTAGTATTTCATGTTCTTTCTT
 TTTTAAAAATGGTATGCTTAGAACTAATTAAGATTAGATTAGATTAGATTAGAAAATAATC
 AGAGAGGGATTGATGAATGCTAAAGCATCATGAAAAATTCAAAATTTTTGCTTCTAATT
 CAGAAATCAATTAATTCATATTACTATAAAAGACAGCAGCCAGATGTGTGCCAGCTGAG
 GAGTGATAAACTGTGTAACGTGAGTGCTATGTAGAAACAGAAAGGAGTGAAGGGTTGA

TGTGCGCTGCAACATCTTGAAAACATTCGGCTACATGATGGAAGCCAGGCACAAAAAGCC
ACATATTGCATGGTTATGTTTATATGAAATGTTTAAAAATACATGGATTCTTAGCAAAACAGA
GTAAGATGTTACTTAGGGTCAGGAAAAGATTAAAAAATACTATTGATGTGGAATG
ATCTTAATTTGGGGAAAAGACAATTTCTAAGACGAAATAGTTGAGGTAGATATAGTTAT
ATCCCTGTGGATATTGTAATAAACAGCATGCTGTGCTCTGAGAAGGGCCTAATGAAGGG
GCAGGAGGAAAGTGAAATGAGATGGTAGAAAGGAAAGTCATATAACCATGGCTTCTCTCGTG
GGTGGAATCTAGATATGTTAATATATTGACATAAAGGAAGGAATTGTTTAGGGAAGGATC
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TGTGTGTGGAGACACCATAATAAACTCCTTTTTTGTGTTGCTAACTAAAACCACTAAAATC
TAAAAACAAAACATTTTTGCACAAGAATTATTTATTATTCAATAAAGATGTTTAAATGGGG
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AATCCAATCCAGGGCATGATGCTTACTCCTACACAGAACTAAAGATTAAAGAGAGTTTAA
AAGTAACCATGACATCTCTCTGTTCTTTAGCGATAAGTTCTTAATATTTATGGCTGCTTGT
GTATGTTCTAATTTCTCTAATATTGTGCATTTAGTTGGCAACTACTTTGTTTGAATTGAGT
TGGAGTTAAGGTCCCATAGGATTAATCTCAACATATTTCTATATTTATAAACTTTTCTCTCT

Exon 4 ? (Nuc 11286) ↓

TTGTGAAAGTTCCTTTGAGAAAACAAATATGCCCATATCTTTCTTTACAGGTCTTAAAAATG
AGCTATAACAAAGTCCAAATAATTGAGAAGGATACTTTGTATGGACTCAGGAGCTTGACCCGG
TTGCACCTGGATCACAACAACATTGAGTTTATCAACCCCGAGGCGTTTTACGGACTCACCTTGC
TCCGCTTGGTACATCTAGAAGGAAACCGGCTGACAAAGCTCCATCCAGACACATTGTCTCTTT
GAGCTATCTCCAGATATTTAAAACTCCTTCATTAAGNACCTGTACTGTATGATAACTTCATTG
ACCTCCCTCCAAAAAGAAATGGTCTCCTCTATGCCAAACCTAGAAAGCCTTTACTTGATGGAA
ACCCATGGACCTGTGACTGCCATTTAAAGTGTTGTCCGAGTGGATGCAGGGAAACCCAGGTA

Nuc 11680 ↑

ACTATCTTGTGTTGTTGTTCTTTTTTATARKACGTAATTTCTCAATTTCAATTTAGAATGA
TATCCCAAAAGTCCCCATAACCTCCCCCCCACCTCCCTACCTACCCATTCCCATTTTTTGG
CCCTGGCATTCCCCTGTACTGGGGCATATAAAGTTTGCCTGTCCAATGGACCTCTCTTTCC
AGTGATGGCCAACTAGGCCATCTTTTGATACATATGCAGCTAGAGTCAAGAGCTCTGGGG
TACTGGTTAGTTTCATAATGTTGTTGCACCTACAGGGTTGAA

Nuc 11967 ↑

(SEQ ID NO:3)

Figure 8

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length
1	1	542	542	2356
2	2898	3094	197	1334
3	4428	4557	130	3068
4	7625	8019	394	

Figure 9

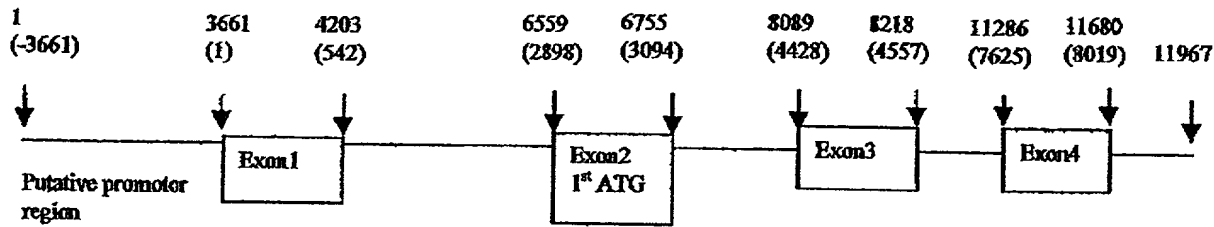


Figure 10

cDNA_rat	1	cgagagacgacagaagggttaaggctgcgagaagacgacagaagggtccag
genomic_hu	1	-----
cDNA_rat	51	aaaaaggaaagtgcctggaggggagtggggacaaaagcagcgaccaagtga
genomic_hu	1	-----
cDNA_rat	101	atgtcacttcagtgactgaggccaggcaaaacgcgcgggaaggattttgt
genomic_hu	1	-----
cDNA_rat	151	gtagcttgggaacctttcatagacactgatgacacgtttacgcaaaatag
genomic_hu	1	-----
cDNA_rat	201	aaatttgaggagaaaacgcctgggccttoggaaaggagtgattgattagta
genomic_hu	1	-----
cDNA_rat	251	cttgcaagtttaggtgactttaaggagaactaactaatgtatactattga
genomic_hu	1	-----
cDNA_rat	301	gggaggaggaagagcattacagagtttccagcagcagcaggaaagctttg
genomic_hu	1	-----
cDNA_rat	351	gttaatttggaatggatgatagcattaaaataacagaagcgccctccagg
genomic_hu	1	-----
cDNA_rat	401	tctotgaagottcagtcctccagctgaaagccagaaaagactaagccac
genomic_hu	1	-----
cDNA_rat	451	taagccttttgatccctttggaagcaagaactttccttcctggggtga
genomic_hu	1	-----
cDNA_rat	501	agactctcctcagaagatttctgtctctgcctatgttacaagaggaatc
genomic_hu	1	-----
cDNA_rat	551	aaaaccaagacagaagagctcaggatgcagggtgagaggcagggaagtacg
genomic_hu	1	-----
cDNA_rat	601	cggottgttgatctccctcactgotgtgtgcotggtggtcaccctggga
genomic_hu	1	-----
cDNA_rat	651	gcagggcctgtcctgcgcgtgtgcctgctatgtgccacagaggtgcac
genomic_hu	1	-----
cDNA_rat	701	tgtacatttoggtacctgacctccatcccagatggcatcccgccaatgt
genomic_hu	1	-----
cDNA_rat	751	ggaacgaataaatttaggatataacagccttactagattgacagaaaacg
genomic_hu	1	-----
cDNA_rat	801	actttgatggcctgagcaaacctggagttactcatgtgcacagtaattggc
genomic_hu	1	-----
cDNA_rat	851	attcacagagtcagtgacaagaccttctcgggcttgagtccttgaggt
genomic_hu	1	-----
cDNA_rat	901	cttaaaaatgagctataacaaagtccaaatcattoggaaggatactttct
genomic_hu	1	-----

cDNA_rat	951	acggactcgggagcttggtccggttgacactggatcacacaacattgaa
genomic_hu	1	-----
cDNA_rat	1001	ttcatcaacctgaggccttttatggacttacctcgctccgcttggtaca
genomic_hu	1	-----
cDNA_rat	1051	tttagaaggaaaccggctcacaaagctccatccagacacatttgctcat
genomic_hu	1	-----
cDNA_rat	1101	taagctatctccagatatttaaacctctttcattaagtacctgttcttg
genomic_hu	1	-----
cDNA_rat	1151	tctgataacttcctgacctccctcccaaaagaaatggtctcctacatgcc
genomic_hu	1	-----
cDNA_rat	1201	aaacotagaaagcctgtatttgcatggaaacccatggacctgtgactgcc
genomic_hu	1	-----
cDNA_rat	1251	atttaaagtgggtgtotgagtggatgcagggaacccagatataataaaa
genomic_hu	1	-----
cDNA_rat	1301	tgcaagaagacagaagctcttcagtcctcagcaatgtcccctttgcat
genomic_hu	1	-----
cDNA_rat	1351	gaacccaggatctctaaaggcagaccctttgctatggtaccatctggag
genomic_hu	1	-----
cDNA_rat	1401	ctttcctatgtacaaagccaaccattgatccatcactgaagtoaaagagc
genomic_hu	1	-----
cDNA_rat	1451	ctggttactcaggaggacaatggatctgcctccacctcacctcaagattt
genomic_hu	1	-----
cDNA_rat	1501	catagaaccccttggtccttctgtctttgaacatgacanannntctggaa
genomic_hu	1	-----
cDNA_rat	1551	ataaggccgacatggtctgtagtatccaaaagccatcaaggacatcacca
genomic_hu	1	-----
cDNA_rat	1601	actgcattcactgaagaaaatgactacatcatgotaaatgcgtcattttc
genomic_hu	1	-----
cDNA_rat	1651	cacaaatcttgtgtgcagtgtagattataatcacatccagccagtggtggc
genomic_hu	1	-----
cDNA_rat	1701	aaottctggctttatacagtgactctcctctgatactagaaaggaagccc
genomic_hu	1	-----
cDNA_rat	1751	cagcttaccgagactccttcactgtcttctagatataaacagggtggctct
genomic_hu	1	-----
cDNA_rat	1801	taggcctgaagacattttaccagcatagaggctgatgtcagagcagacc
genomic_hu	1	-----
cDNA_rat	1851	ctttttggttccaacaagaaaaattgtcttcagctgaacagaactgcc
genomic_hu	1	-----
cDNA_rat	1901	accacacttagcacattacagatccagttttccactgatgtcctaaatcgc
genomic_hu	1	-----
cDNA_rat	1951	tttaccaagggcggagatgagagcggagagactcaaattggaccatgatcc
genomic_hu	1	-----

cDNA_rat	2001	tgatgatgaacaatccaaaactggaaogcaactgtcctggttggcggcact
genomic_hu	1	-----
cDNA_rat	2051	attgccctgagctgtccaggcaaaggcgacccttcacctcacttggaatg
genomic_hu	1	-----
cDNA_rat	2101	gottotagctgatgggagtaaagtgagagccccttacgttagogaggatg
genomic_hu	1	-----
cDNA_rat	2151	ggcgaatcctaataagacaaaaatgggaagttggaactgcagatggctgac
genomic_hu	1	-----
cDNA_rat	2201	agctttgatgcaggtotttaccactgcataagcaccaatgatgcagatgc
genomic_hu	1	-----
cDNA_rat	2251	ggatgtttcacatacaggataactgtggttagagccctatggagaaagca
genomic_hu	1	-----
cDNA_rat	2301	cacatgacagtggagtccagcacacagtgggttacgggtgagacgctcgac
genomic_hu	1	-----
cDNA_rat	2351	cttccatgcctttccacgggtgttcagatgcttotattagctggattct
genomic_hu	1	-----
cDNA_rat	2401	tccagggaaactgtgttctctcagccatcaagagacaggcaaattctta
genomic_hu	1	-----
cDNA_rat	2451	acaatgggaccttaagaatattacaggttacgcacaaagatcaaggtcat
genomic_hu	1	-----
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genomic_hu	1	-----
cDNA_rat	2551	agtttcagttcaaaagaaaggccaaaggatgggttagcatgacaggagg
genomic_hu	1	-----
cDNA_rat	2601	cagggtgatctggacttgagaaacccactccagtgtttcccttaagcag
genomic_hu	1	-----
cDNA_rat	2651	ccagcatctttgaaactctctgcatcagctttgacagggtcagaggctgg
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genomic_hu	1	-----
cDNA_rat	2851	tctagaaaaagccaaaaagaattctgtgccaaaaagcaagaaaatacca
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genomic_hu	1	-----
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genomic_hu	1	-----

cDNA_rat	3001	gaaaactaaggcttctggtgtccocaggaaggtcaccaactgctgactctg
genomic_hu	1	-----^-----
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genomic_hu	1	-----
cDNA_rat	3851	aatgttggggtcatagcagaagagtctaccactgtggtcaagaaaccaact
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genomic_hu	1	-----
cDNA_rat	4051	caatagtggtcacctgagcatgcoctgggaccatccaaactgggaaagatt
genomic_hu	1	-----
cDNA_rat	4101	cagtggaacaacaccacttcccagcccccctcagcacacccctcaataoca
genomic_hu	1	-----

cDNA_rat	4151	acaagcacaaaattctcaaagaggaaaactccottgcaccagatctttgt
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cDNA_rat	4201	aaataaccagaagaaggaggggatgttaagaatccatatcaattoggtt
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cDNA_rat	4251	tacaaaagaaccagccgcaagcttccaaaatagctcctcttttacct
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cDNA_rat	4301	acaggtcagagttcccccagattctacaactctcttgacaagtcgoc
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cDNA_rat	4701	ccccottggcttttcagtcattccccacgacaagatgatgggtggaatgta
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cDNA_rat	4751	agtgcagttgcttatcaactcaacaacotctcttctggccataactgaact
genomic_hu	1	-----
cDNA_rat	4801	gtttgagaagtaaccccagactttgggaataacaacagctttggaacaa
genomic_hu	1	-----
cDNA_rat	4851	cgttggtgagcaaatcacaggagagtaccacagtgaaaagagcctcagac
genomic_hu	1	-----
cDNA_rat	4901	acaccaccaccactcctcagcagtggggggccccagtgcccactccttc
genomic_hu	1	-----
cDNA_rat	4951	cccacctccttttactaagggtgtggttacagacagcaaagtcacatcag
genomic_hu	1	-----
cDNA_rat	5001	ctttccagatgaogtcaaataagagtggtcaccatatatgaatcttcaagg
genomic_hu	1	-----
cDNA_rat	5051	cacaatacagatctgcagcaacccctcagcagaggttagccccaatcctga
genomic_hu	1	-----
cDNA_rat	5101	gatcataactggaaccactgactctccctctaattctgtttccatccactt
genomic_hu	1	-----
cDNA_rat	5151	ctgtgccagcactaagggtagataaaccacagaattctaaatggaagccc
genomic_hu	1	-----
cDNA_rat	5201	tctccctggccagaacacaaaatatcagctcaagtcatactccgaaacct
genomic_hu	1	-----

cDNA_rat	5251	tgagaagggcaaaaggccagcagtaagcatgtccccccacctcagccttc
genomic_hu	1	-----
cDNA_rat	5301	cagaggccagcactcatgcctcacactggaatacacagaagcatgcagaa
genomic_hu	1	-----
cDNA_rat	5351	aagagtgtttttgataagaaacctgggtcaaaacccaacttccaaacatct
genomic_hu	1	-----
cDNA_rat	5401	gccttacgtctctctacctaagactctattgaaaaagccaagaataattg
genomic_hu	1	-----
cDNA_rat	5451	gagaaagggtgcaagctttacagttccagctaattcagaogtttttctt
genomic_hu	1	-----
cDNA_rat	5501	ccttgtaggggtgttggagacccactgcccacatccactggaccagagt
genomic_hu	1	-----
cDNA_rat	5551	ttcatcagganttgaaatatccaagggacacagaaaagccggttccacg
genomic_hu	1	-----
cDNA_rat	5601	tgottcccaatggcaccttgtccatccagaggggcagtattcaggaccgt
genomic_hu	1	-----
cDNA_rat	5651	ggacagtacctgtgctctgcatttaatccactgggcgtagaccattttca
genomic_hu	1	-----
cDNA_rat	5701	tgtctotttgtctgtgtgttttttaccggcaaggattttggacagacatg
genomic_hu	1	-----
cDNA_rat	5751	tcaaggagatcacagttcactttggaagtactgtggaactaaagtcaga
genomic_hu	1	-----
cDNA_rat	5801	gtggaggggtatgccgaggcctacggtttcctggatacttgcaaaccaaac
genomic_hu	1	-----
cDNA_rat	5851	ggtggtctcagaaacggccaagggaagcagaaaggtctgggtaaacacctg
genomic_hu	1	-----
cDNA_rat	5901	atggaacattgatcatctataatctgagtcctttatgatcgtgggttttac
genomic_hu	1	-----
cDNA_rat	5951	aagtgtgtggccagcaacccatctggccaggattcactgttggttaagat
genomic_hu	1	-----
cDNA_rat	6001	acaagtcacacagctccccctgtcattatagagcaaaagaggcaagcca
genomic_hu	1	-----
cDNA_rat	6051	tcgttgggggttttaggtggaagtttgaaactgcctgcactgcaaaagga
genomic_hu	1	-----
cDNA_rat	6101	actccccagcctagtgttcactgggtcctttatgatgggactgaactaaa
genomic_hu	1	-----
cDNA_rat	6151	accattgcagttgactcattccagatttttctgtatccaaatggaactc
genomic_hu	1	-----
cDNA_rat	6201	tgtatataagaagcatogctccttcagtgaggggcacttatgagtgcatt
genomic_hu	1	-----
cDNA_rat	6251	gccaccagctcctcaggctcagagagaagggtagtgattcttactgtgga
genomic_hu	1	-----

rat	7351	CttTGGAAGCAGAGTCACGGTCCATCCAAATGGAACCTTGGAgatgagga
.c_hu	890	CtatGGAAGCAGAATCAGTCCATAAAATGGAACCTTGGaattagga
rat	7401	acatccGGCTTTCTGACTCTGCGGACTTCACCTGTGTGGttcggagcgag
.c_hu	940	atgtgaGGCTTTTCAGATTACGCCGACTTTATCTGTGTGGcccgaaatgaa
rat	7451	ggaGGAGAGAGTGTGTGGTAGTGCAGTTAGAAGTCTAGAAATGCTGAG
.c_hu	990	ggtGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTACTGGAATGCTGAG
rat	7501	AAGACCAACATTTCAGAAACCCATTCAACGAAAAgtcatcgcccaagctg
.c_hu	1040	AAGACCGACATTTAGAAATCCATTTAATGAAAAaatagttgcccagctgg
rat	7551	gcaagcccgtagCACTGAACTGCTCTGTGGATGGGAACCCCCACCTGAA
.c_hu	1090	gaaagtccacAGCATGAATTGCTCTGTGTGATGGTAACCCACCACCTGAA
rat	7601	attacCTGGATCTTACCTGACGGCACACAGTTTGCTAACAGACCAcaaaa
.c_hu	1140	ataatCTGGATTTTACCAAATGGCACACGATTTTCCAATGGACCAcaaaag
rat	7651	ttccccGTATCTGATGGCAGGCAATGGCTCTCTCATCCTTTACAAAgcaa
.c_hu	1190	ttatcagTATCTGATAGCAAGCAATGGTTCTTTTATCATTTCTAAaacia
rat	7701	ctcggaaacaagtCAGGGAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGC
.c_hu	1240	ctcgggaggatgCAGGAAAATATCGCTGTGCAGCTAGGAATAAGGTTGGC
rat	7751	TAcategagaaactcatcctgttagagATTGGGCAGAAGCCAGTCATTCT
.c_hu	1290	TAtattgagaaattagtcattattagaaATTGGCCAGAGCCAGTTATTCT
rat	7801	GACATACGAACCCAGGGatggtgaagagcgTCAGTGGGGAACCGTTATCAC
.c_hu	1340	TACCTATGCACCCAGGGAcagtaaaaggoaTCAGTGGAGAATCTCTATCAC
rat	7851	TGCATTGTGTGTCTGATGGgATCCCCAAGCCAAATGTCAAAGTGGACTACA
.c_hu	1390	TGCATTGTGTGTCTGATGGaATCCCTAAGCCAAATATCAAATGGACTATG
rat	7901	CCGGGTGGccATGTAATCGACAGGCCTCAAGTGGATGGAAAATACATAcT
.c_hu	1440	CCAAGTGGttATGTAGTAGACAGGCCTCAAATTAATGGGAAATACATatT
rat	7951	GCATGAAAATGGCACGCTGCTCATCAAAGCAACAACAGCtcaagaccaAG
.c_hu	1490	GCATGACAATGGCACCTTAGTCATTAAAGAAGCAACAGCttatgacagAG
rat	8001	GAAATTATATCTGTAGGGCTCAAACAGTGTGGCCAggcagttattagc
.c_hu	1540	GAAACTATATCTGTAAGGCTCAAATAGTGTGGTCatatactgattact
rat	8051	gtgtCAGTGATGGTTGTGGCCTACCTCCCCGAATCATAAactacctACC
.c_hu	1590	gttcCAGTAATGATTGTAGCTACCTCCCCGAATTACAAatogtccACC
rat	8101	CAGGAACATGCTCAGGAGGACAGGGGAAGCCatgCAGCTCCACTGTGTGG
.c_hu	1640	CAGGAGTATTGTCAACAGGACAGGGGCAGCctttCAGCTCCACTGTGTGG
rat	8151	CCTTGGAATCCCCAAGCCaaAAGTCAOCTGGGAGACGCCAAGACACTCC
.c_hu	1690	CCTTGGGAGTTCCCAAGCCagAAATCACATGGGAGATGCCCTGACCACTCC
rat	8201	CTGCTCTCAaaagcaacagcaagaaaacccCATAGAAGTGAGATGCTTCA
.c_hu	1740	CTTCTCTCAAcggcaagtaagagaggacaCATGGAAGTGAGCAGCTTCA
rat	8251	CCCACAAGGTACGCTgGTCATTTCAGAACTCTCCAAACCTCGGATTCCGGag
.c_hu	1790	CTTACAAGGTACCTtaGTCATTTCAGAACTCCCAAACTCCGATTCTGGga
rat	8301	tctATAAGTGCAGAGCTCAGAACCTACTTGGgacTGATTACGCAACAACT
.c_hu	1840	taTACAAATGCACAGCAAGAACCCTTGGtagTGATTATGCAGCAACG
rat	8351	TACATCCAGGTACTCTGACAGGAaggggagactaaaattoaacagaagt
.c_hu	1890	TATATTCAAGTAATCTGACATGAAataataaagtcacaacatctgggca

cDNA_rat	8401	ccacatccacagggTTATTTTGGAGAAGTTAATCAAAGGCAGCCA
genomic_hu	1940	gaa-----TTATTTTGGAGAAGTTAATCAAAGGCAGCCA
cDNA_rat	8451	TAGGCATGTAAATGagtcTGAATACATTACAGTATTAAATTTACAATGG
genomic_hu	1979	TAGGCATGTAAATGAattTGAATACATTACAGTATTAAATTTACAATGA
cDNA_rat	8501	ACATGCgatga-----GACTTGTAATGAAAGCATTGTGAAC TGaaaccg
genomic_hu	2029	ACATGCaaaataaaaagGACTTGTAATAAATGCATTATGAAC TGatgata
cDNA_rat	8546	agtctctg-----TGGATCTCAAAGCAAACCTCTTAACTTAAGGCACTTTg
genomic_hu	2079	ctgatttattttaTGGATCTCAAACAAACCTTTTAACTTAAGGCACTTTt
cDNA_rat	8591	ATTTTGCCAACAAATAATAACAAACattaagagaaaaaatgacCACTA
genomic_hu	2129	ATTTTGCCAACAAATAACAATAACAaacattgaaacggtt----CACTA
cDNA_rat	8641	CGAAATAACAAACGGCTAATGCACCTGAATTctcagtaaaaaagaccttc
genomic_hu	2175	TAAATAACAAATGGCTAATGTACCTGAATTtttcagtaaaaaaatgaac
cDNA_rat	8691	tctcgctaacagttgCCAGCTGCCTCGTGTCTGTTTCTACCAATGTCAC
genomic_hu	2225	ttctaata-----CCAGTTGCCTAGTGTCCACCTCCTATCAATGTTAC
cDNA_rat	8741	AAACatogcacacagggTGATGGAGTCAACGGGAAAGATTAAAGTTTGCG
genomic_hu	2268	AAGCATggcactca----GAACAGAGACAATGGAAATATTAAATCTGCA
cDNA_rat	8791	GTCTgtgtaaatctca-----ATGTACAAATATTCTGtcncTG
genomic_hu	2314	ATCtttatgatgtaaatattaccatcctgATGTATAAATATTTTG----TG

exon1 (2342-2397)

cDNA_rat	8791	GTCTgtgtaaatctca-----ATGTACAAATATTCTGtcncTG
genomic_hu	2314	ATCtttatgatgtaaatattaccatcctgATGTATAAATATTTTG----TG
cDNA_rat	8829	GTTTATAACATTTTGATAAAACCGAAAAAAAAAAAAAAAAAAAAA
genomic_hu	2360	GTTTATAAATTTTTTGCTAAAACCTACAGAAAATAAGcactgaactgtc

(Genomic human OCP: SEQ ID NO:4)
(cDNA rat: SEQ ID NO:5)

Figure 11

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length	Remarks
1	1	208	208	69	No valid splice site found upstream this exon
2	277	429	153	18	
3	447	485	39	1561	
4	2046	2244	199	1351	
5	3595	3724	130	3254	
6	6978	7359	382	4123	
7	11482	14903	3422	38	
8	14941	15307	367	51	
9	15358	15825	468	1039	
10	16864	~17760	~897	?	Last exon might be complete
11	?(1)	2317	~231 7	25	Exon is not complete and start site is not known
12	2342	2397	56	-	

Fig 12.

608 Human translated nucleotide sequence (ORF)

ATGAAGGTAAAAGGCAGAGGAATCACCTGCTTGGTCTCCTTTGCTGT
GATCTGCCTGGTCGCCACCCCTGGGGGCAAGGCCTGTCTCGCCGCTGTG
CCTGTTATATGCCTACGGAGGTACACTGCACATTTGGGTACCTGACTTCCA
TCCCAGACAGCATCCCGCCAATGTGGAACGCATCAATTTAGGATACAAC
AGCTTGGTTAGATTGATGGAAAACAGATTTTTCTGGCCTGACCAAACCTGGA
GTTACTCATGCTTCACAGCAATGGCATTACACAATCCCTGACAAGACCTT
CTCAGATTTGCAGGCCTTGCAGGTCTTAAAAATGAGCTATAATAAAGTCC
GAAAACTTCAGAAAGATACTTTTTATGGCCTCAGGAGCTTGACACGATTG
CACATGGACCACAACAATATTGAGTTTATAAACCCAGAGGTTTTTATGG
GCTCAACTTTCTCCGCCTGGTGCACCTGGAAGGAAATCAGCTCACTAAGCT
CCACCCAGATACATTTGTCTCTTTGAGCTACCTCCAGATATTTAAATCTC
TTTCATTAAGTTCCTATACTTGTCTGATAACTTCCTGACCTCCCTCCCTCAA
GAGATGGTCTCCTATATGCCTGACCTAGACAGCCTTTACCTGCATGGAAA
CCCATGGACCTGTGATTGCCATTTAAAGTGGTTGTCTGACTGGATACAGCC
AGATGTAATAAAATGCAAAAAGATAGAAGTCCCTCTAGTGCTCAGCAGT
GTCCACTTTGCATGAACCTAGGACTTCTAAAGGCAAGCCGTTAGCTATG
GTCTCAGCTGCAGCTTCCAGTGTGCCAAGCCAACCATTGACTCATCCCTG
AAATCAAAGAGCCTGACTATTCTGGAAGACAGTAGTTCTGCTTTCATCTCT
CCCCAAGGTTTCATGGCACCCCTTTGGCTCCCTCACTTTGAATATGACAGAT
CAGTCTGGAAATGAAGCTAACATGGTCTGCAGTATTCAAAAGCCCTCAAG
GACATCACCCATTGCATTCACTGAAGAAAATGACTACATCGTGCTAAATA
CTTCATTTCAACATTTTGGTGTGCAACATAGATTACGGTCACATTTCAGC
CAGTGTGGCAAATTTTGGCTTTGTACAGTGATTCTCTCTGATAGTAA
GGAGCCACTTGCTTAGTGAAACACCGCAGCTCTATTACAAATATAAACAG
GTGGCTCCTAAGCCTGAAGACATTTTACCAACATAGAGGCAGATCTCAG
AGCAGATCCCTCTTGGTTAATGCAAGACCAAATTTCTTGCAGCTGAACA
GAACTGCCACCACATTCACTACATTACAGATCCAGTACTCCAGTGATGCT
CAAATCACTTTACCAAGAGCAGAGATGAGGCCAAGTGAAACACAAATGGA
CTATGATTTCAAGGGATAACAATACTAAGCTGGAACATACTGTCTTGGTA
GGTGGAAACCGTTGGCCTGAAGTCCCAGGCCAAGGAGACCCCAACCCACA
CGTGGATTGGCTTCTAGCTGATGGAAGTAAAGTGAGAGCCCTTATGTCA
GTGAGGATGGACGGATCCTAATAGACAAAAGTGGAATTTGGAATCCA
GATGGCTGATAGTTTGTACACAGGCGTATATCACTGTATAAGCAGCAATT
ATGATGATGCAGATATTCTCACCTATAGGATAACTGTGGTAGAACCTTTGG
TCGAAGCCTATCAGGAAAATGGGATTCTACACACAGTTTTTCATTGGTGAA
ACACTTGATCTTCCATGCCATTCTACTGGTATCCCAGATGCCTCTATTAGC
TGGGTATTCCAGGAAACAATGTGCTCTATCAGTCATCAAGAGACAAGAA
AGTTCTAAACAATGGCACATTAAGAATATTACAGGTCAACCCGAAAGACC
AAGGTTATTATCGCTGTGTGGCAGCCAACCCATCAGGGGTTGATTTTTTGA
TTTTCCAAGTTTCAGTCAAGATGAAAGGACAAAGGCCCTTGGAGCATGAT
GGAGAAACAGAGGGATCTGGACTTGATGAGTCCAATCCTATTGCTCATCT
TAAGGAGCCACCAGGTGCACAACCTCCGACATCTGCTCTGATGGAGGCTG
AGGTTGGAAAACACACCTCAAGCACAAAGTAAGAGGCACAACATATCGGGA
ATTAACACTCCAGCGACGTGGAGATTCAACACATCGACGTTTTAGGGAGA
ATAGGAGGCATTTCCTCCCTCTGCTAGGAGAATTGACCCACAACATTGG
GCGGCACTGTTGGAGAAAGCTAAAAAGAATGCTATGCCAGACAAGCGAG
AAAATACCACAGTGAGCCACCCCAAGTGGTCAACCAACTCCCAAACATA
CCTGGTGAAGAAGACGATTCTCAGGCATGCTCGCTCTACATGAGGAATT

TATGGTCCCGGCCACTAAAGCTTTGAACCTTCCAGCAAGGACAGTGACTG
CTGACTCCAGAACAATATCTGATAGTCCTATGACAAACATAAAATTATGGC
ACAGAAATTCTCTCTGTGTGAATTCACAAATACTACCACTGAAGAACCC
ACAGATTCAAACGTCTACTGCTATTAACACTACAGCCATGTCAAAGAA
TATAAACCCCAACCATGTCAAGCCAAATACAAGGCACAACCAATCAACATT
CATCCACTGTCTTTCCACTGCTACTTGGAGCAACTGAATTTTCAGGACTCTG
ACCAGATGGGAAGAGGAAGAGAGCATTTCCAAAGTAGACCCCAATAAC
AGTAAGGACTATGATCAAAGATGTCAATGTCAAATGCTTAGTAGCACCA
CCAACAAACTATTATTAGAGTCAGTAAATACCACAAATAGTCATCAGACA
TCTGTAAGAGAAGTGAGTGAACCCAGGCACAATCACTTCTATTCTCACAC
TACTCAAATACTTAGCACCTCCACGTTCCCTTCAGATCCACACACAGCTGC
TCATTCTCAGTTTCCGATCCCTAGAAATAGTACAGTTAACATCCCGCTGTT
CAGACGCTTTGGGAGGCAGAGGAAAATTGGCGGAAGGGGGCGGATTATC
AGCCCATATAGAACTCCAGTTCTGCGACGGCATAGATACAGCATTITCAG
GTCAACAACCAGAGGTTCTTCTGAAAAAAGCACTACTGCATTCTCAGCCA
CAGTGCTCAATGTGACATGTCTGTCTGTCTTCCAGGGAGAGGCTCACCA
CTGCCACAGCAGCATTGTCTTTTCCAAGTGCTGCTCCCATCACCTTCCCCA
AAGCTGACATTGCTAGAGTCCCATCAGAAGAGTCTACAACCTTAGTCCAG
AATCCACTATTACTACTTGAGAACAACCCAGTGATAGAGAAAAACAACCC
CACAAATAAAATATTTTCAGGACTGAAATTTCCCAAGTGACTCCAACCTGGT
CAGTCATGACATATGCTCCAACATCCATACCCATGGAAAAAACTCACAAA
GTAAACGCCAGTTACCCACGTGTGTCTAGCACCAATGAAGCTAAAAGAGA
TTCAGTGATTACATCGTCACTTTTCAGGTGCTATCACCAGCCACCAATGAC
TATTATAGCCATTACAAGGTTTTCAAGAAGGAAAATTCCTGGCAACAGA
ACTTTGTAAATAACCATAACCCAAAAGGCAGATTAAGGAATCAACATAAA
GTTAGTTTACAAAAAAGCACAGCTGTGATGCTTCTTAAACATCTCTGCT
TTACCACAGAGACAAAGTTCCCTTTCCATTTACCCACACTTTCAACAAGT
GTGATGCAAAATTCATCTAATACTTGACTACCGCTCACCACACTACGACC
AAAACACACAATCCTGGAAGTCTTCCAACAAAAGAGGAGCTTCCCTTCCC
ACCCCTTAACCCTATGCTTCTTAGTATTATAAGCAAAAGACTCAAGTACAA
AAAGCATCATATCAACGCAACAGCAATACCAGCAACAACCTCTACCTTC
CCTGCATCTGTCACTTATGAAACCCAAACAGAGAGATCTAGAGCACA
AACAATACAAAGAGAACAGGAGCCTCAAAAAGAAGAACAGGACTGACCCA
AACATCTCTCCAGACCAGAGTTCTGGCTTCACTACACCCACTGCTATGACA
CCTCCTGCTCTGGCATTCACTCATTCCCCACCAGAAAACACAACCTGGGATT
TCAAGCACAAATCAGTTTTTCATTCAAGAAGCTCTTAATCTGACAGATGTGATT
GAAGAACTAGCCCAAGCAAGTACTCAGACTTTGAAGAGCACAATTGCTTC
TGAAACAACCTTTGTCCAGCAAATCACACCAGAGTACCACAACCTAGGAAAG
CATCATTAGACACTCCCATACCACCATCTTGAGCAGCAGTGCTACTCTAA
TGCCAGTTCCCATCTCCCTCCCTTTACTCAGAGAGCAGTTACTGACACAC
GTGGCGACTCCCATTTCCGGCTTATGACAAATACAGTGGTCAAGCTGCAC
GAATCCTCAAGGCACAATCTCCAATGCCAAGTTCACAATTGGAACCACT
CACTTCATCTACCTCTAATCTGTTACATTCTACTCCCATGCCAGCACTAAC
AACAGTTAAATCACAGAATTCCAAATTAAGTCCATCTCCCTGGGCAGAAAT
ACCAATTTTGGCACAACCATACTCAGACATTGCTGAAAAAGGCAAAAAG
CCAGAAGTAAGCATGTTGGCTACTACAGGCTGTCCGAGGCCACCACTCT
TGTTTCAGATTGGGATGGACAGAAGAACAACAAAGAGTGACTTTGATA
AGAAACCAGTTCAAGAAGCAACAACCTTCCAAACTCCTTCCCTTTGACTCTT
TGTCTAGGTATATATTTGAAAAGCCCAGGATAGTTGGAGGAAAAGCTGCA
AGTTTTACTATTCCAGCTAACTCAGATGCCTTTCTTCCCTGTGAAGCTGTT

GGAAATCCCCTGCCACCATTTCATTGGACCAGAGTTTCAGGACTTGATTTA
TCTAGAGGAAACCAGAATAGCAGGGTCCAGGTTCTCCCAATGGTACCCT
GTCCATCCAGAGGGTGGAAATTCAGGACCGCGGACAGTACTTGTGTCCG
CATCCAATCTGTTTGGCACAGACCACCTTCATGTCACCTTGTCTGTGGTT
CCTATCCTCCCAGGATCCTGGAGAGACGTACCAAAGAGATCACAGTTCAT
TCCGGAAGCACTGTGGAAGTGCAGAGCAGAAGGTAGGCCAAGCC
CTACAGTTACCTGGATTCTTGCAAACCAACAGTTGTCTCAGAATCATCCC
AGGGAAGTAGGCAGGCTGTGGTGACGGTTGACGGAACATTGGTCTCCAC
AATCTCAGTATTTATGACCGTGGCTTTTACAAATGTGTGGCCAGCAACCCA
GGTGGCCAGGATTCAGTCTGGTTAAAATACAAGTCATTGCAGCACCACC
TGTTATTCTAGAGCAAAGGAGGCCAAGTCATTGTAGGCACCTGGGGTGAAA
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GGGTCTCTCTGATGGCACTGAAAGTGAACCAATTACAGTTTACCAATCCA
AGTTGTTCTTATTTCAAATGGGACTTTGTATATAAGAAACCTAGCCTCTT
CAGACAGGGGCACTTATGAATGCATTGCTACCAGTTCCACTGGTTCGGAG
CGAAGAGTAGTAATGCTTACAATGGAAGAGCGAGTGACCAGCCCCAGGA
TAGAAGCTGCATCCCAGAAAAGGACTGAAGTGAATTTGGGGACAAATTA
CTACTGAACTGCTCAGCCACTGGGGAGCCCCAACCCAAATAATGTGGAG
GTTACCATCCAAGGCTGTGGTCGACCACTGGAGCTGGATCCACGTCATCC
CTAATGGATCCCCTGTTTATTGGATCAGTAACAGAAAAAGACAGTGGTGTC
TACTTGTGTGTGGCAAGAAACAAAATGGGGGATGATCTGATACTGATGCA
TGTTAGCCTAAGACTGAAACCTGCCAAAATTGACCACAAGCAGTATTTTA
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GGCTCCCCAGTGCCAGAGATATCTTGGAGTTTGCCTGATGGAACCATGAT
CAACAATGCAATGCAAGCCGATGACAGTGGCCACAGGACTAGGAGATAT
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TGTAGCCCAGAAATCCCAAGTGGGGATGACACCAAAATGTACAACTGGATG
TGGTCTCTAAACCTCCATTAATCAATGGTCTGTATACAAACAGAACTGTTA
TTAAAGCCACAGCTGTGAGACATTCCAAAAAACACTTTGACTGCAGAGCT
GAAGGGACACCATCTCCTGAAGTCATGTGGATCATGCCAGACAATATTTT
CCTCACAGCCCCATACTATGGAAGCAGAATCACAGTCCATAAAAAATGGAA
CCTTGGAAATTAGGAATGTGAGGCTTTCAGATTACAGCCGACTTATCTGTG
TGGCCCCGAAATGAAGGTGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTA
CTGGAATGCTGAGAAGACCGACATTTAGAAATCCATTTAATGAAAAAT
AGTTGCCCAGCTGGGAAAGTCCACAGCATTGAATTGCTCTGTTGATGGTA
ACCCACCACCTGAAATAATCTGGATTTTACCAATGGCACACGATTTTCCA
ATGGACCACAAAGTTATCAGTATCTGATAGCAAGCAATGGTCTTTTATCA
TTTCTAAAACAACTCGGGAGGATGCAGGAAAATATCGTGTGCAGCTAGG
AATAAAGTTGGCTATATTGAGAAATTAGTCATATTAGAAATTGGCCAGAA
GCCAGTTATTCTTACCTATGCACCAGGGACAGTAAAAGGCATCAGTGGAG
AATCTCTATCACTGCATTGTGTCTGATGGAATCCCTAAGCCAAATATCA
AATGGACTATGCCAAGTGGTTATGTAGTAGACAGGCCTCAAATTAATGGG
AAATACATATTGCATGACAATGGCACCTTAGTCATTAAGAAGCAACAGC
TTATGACAGAGGAACTATATCTGTAAGGCTCAAAATAGTGTGGTCATA

CACTGATTACTGTTCCAGTAATGATTGTAGCCTACCCCTCCCCGAATTACAA
ATCGTCCACCCAGGAGTATTGTCACCAGGACAGGGGCAGCCTTTTCAGCTC
CACTGTGTGGCCTTGGGAGTTCCTCAAGCCAGAAATCACATGGGAGATGCG
TGACCACTCCCTTCTCTCAACGGCCAAGTAAAGAGGAGCACATGGAAGTG
AGCAGCTTCACTTACAAGGTACCTAGTCATTAGAATCCCCAAACCTCC
GATTCTGGGATATACAAATGCACAGCAAAGAACCCACTTGGTAGTGATTA
TGCAGCAACGTATATTCAAGTAATCTGA

Figure 13

A

Region			Region Length	% identity	% positives	% gaps
General	Rat	Human				
1-655	1-655	1-653	655	76	86	0
656-726	656-726	654-724	71	46	62	0
727-779	727-779	725-777	53	77	86	0
780-1634	780-1617	778-1612	655	38	53	4
1635-end	1618-end	1613-end	980	74	85	0
	Total	Alignment	2614	62	74	1

B

Region			% identity	% positives	% gaps
Rat	Mouse	Length			
1-238	1-238	238	91	92	1

C

Region			Region Length	% identity
General	Rat	Human		
1-1965	1-1965	1-1965	1965	83
1966-2178	1966-2178	1966-2178	213	86
2179-2337	2179-2337	2179-2337	159	86
2338-4893	2338-4893	2338-4863	2565	63
4894-7833	4852-7791	4864-7761	2940	80
	Total	Alignment	7842	80

D

Region			Region Length	% identity
General	Rat	Mouse		
1-720	1-718	1-720	720	93

Figure 14

```

rat_cDNA      CGAGAGACGACAGAAGGTTACGGCTGCGAGAAGACGACAGAAGGGTCCAGAAAAAGGAAA
human_5+3_corrected
mus_cDNA_5    -----CAGAAGGGTCCAGGAAA-GGAAA

rat_cDNA      GTGCTGGAGGGGAGTGGGACAAAAGCAGCGACCAAGTGAATGTCACTTCAGTGACTGAG
human_5+3_corrected
mus_cDNA_5    GTACTGGAGGGGAGTTGGGACAAAAGCAGCGACCAAGGGACATCGCTTCAGTGACTGAA

rat_cDNA      GCCAGGCCAAAACGCGCGGAAGGATTTTGTGTAGCTTGGGACCCCTTCATAGCACTGAT
human_5+3_corrected
mus_cDNA_5    GCCAGGCCAAAAGGAGCGGGAAGGATTATATGTAGCCTGGGACGCTTCATAAACACTGAT

rat_cDNA      GACACGTTTACGCAAAATA-GAAATTTGAGGAGAAACGCCCTGGGCCTTCGGAAAG---GA
human_5+3_corrected
mus_cDNA_5    GACGTGTTTGTGCAAGCAAGCAATTTGAGGAGAAACGCCCTGGGACGTCCGAAAGAAGGA

rat_cDNA      GTGATTGATTAGTACTTCCAAGTTTAGGTGACTTTAAGGAGAACTAACTAATGTATACTA
human_5+3_corrected
mus_cDNA_5    GTGATCGATTAGTACTTGTAGTTTAGGTGAGTTT--GAGAACTAACTAACCTATACTA

rat_cDNA      TTGAGGGAGGAGGAAGAGCATTACAGAGTTTCCAGCAGCAGCAGGAAGCTTTGGTTAAT
human_5+3_corrected
mus_cDNA_5    TTGAGGGAGGAAGGAAGAGCATT-----CCAGCAGCAGCAGGAAGCTTTGGTTAGT

rat_cDNA      TTGGAATGGATGATAGCATTAAATAACAGAAGCGCCTCCAGGTCTCTGAAGCTTCAGT
human_5+3_corrected
mus_cDNA_5    TTGGAATGTATGATACCATTAAATAACAGAAGCGCCTCCAGTTCTCTGAAGAGTCAGT

rat_cDNA      CCCCAGCTGAAAGCCAGAAAAGACTAAGCCCACTAAGCCTTTTGATCCCTTTGGAAGCA
human_5+3_corrected
mus_cDNA_5    CCCCAGCT-----A-GTGTAGCCTACTAAGCCTTTTGCTCCCGTTGGAAGCA

rat_cDNA      AAGAATTTTCCCTCCCTGGGGTGAAGACTCTCCTCAGAAGATTTCTGTCTCTGCCTATG
human_5+3_corrected
mus_cDNA_5    AAGAACGTTCCCTCAATCAGGTGAAGGCTCTCCTCAGAAGATTTCTGTCTCTGCCTATG

rat_cDNA      TTACAAGAGGAATCAAACCAAGACAGAAGAGCTCAGGATGCAGGTGAGAGGCAGGGAAG
human_5+3_corrected
mus_cDNA_5    TTACAAGAGGATTCAAAGCAAGACAGAAGAGCTCAGGATGCAGAAGAGAGGCAGGGAAG
*** ** * ***** *

rat_cDNA      TCAGCGGCTTGTGTCTCCCTCACTGCTGTCTGCTGGTGGTCAOCCCTGGGAGCAGGG
human_5+3_corrected
mus_cDNA_5    TCACCTGCTTGTCTGGTCTCCTTTGCTGTGATCTGCCTGGTGGCCACCCCTGGGGCAAGG
TCAGCTGCTTGTGTCTCCTCACTGCCATCTGCCTGGTGGTCAOCCCTGGGAGCAGGG
*** * ***** * ***** * ***** * ***** * ***** *

rat_cDNA      CCTGTCTCGCGGCTGTGCTGCTATGTGCCCACAGAGGTGCACTGTACATTCGGTACC
human_5+3_corrected
mus_cDNA_5    CCTGTCTCGCGGCTGTGCTGCTATGTGCCCACAGAGGTGCACTGTACATTCGGTACC
TCTGTCTCGCGGATGTGCTGCTATGTGCCCACAGAGGTGCACTGTACATTCGGGACC
***** ***** * ***** * ***** * ***** * ***** *

rat_cDNA      TGACCTCCATCCAGATGG-CATCCCGCCCAATGTGGAACGAATAAATTTAGGATATAAC
human_5+3_corrected
mus_cDNA_5    TGACTTCCATCCAGACAG-CATCCCGCCCAATGTGGAACGATCAATTTAGGATATAAC
TGACCTCCATCCAGACGGGCATCCAGCCCAATGTGGAACGAGTCAATTTAGGGTATAAC
**** ***** * ***** * ***** * ***** * ***** *

```

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 AGCCTTACTAGATTGACAGAAAACGACTTTGATGGCCTGAGCAAACTGGAGTTACTCATG
 AGCTTGGTTAGATTGATGGAACAGATTTTCTGGCCTGACCAAACTGGAGTTACTCATG
 AGCCTCACTAGATTGACAGAAAATGACTTTCTGGCCTGAGCAGACTGGAGTTACTCATG
 *** * ***** ** * ***** *

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 CTGCACAGTAATGGCATTACACAGAGTCAGTGACAAGACCTTCTCGGGCTTGCACTCTTG
 CTTCACAGCAATGGCATTACACAAATCCCTGACAAGACCTTCTCAGATTGTCAGGCTTG
 CTGCACAGCAATGGCATTACACAGAGTCAGTGACAAGACCTTCTCGGGCTTGCACTCTTG
 ** ***** **

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 CAGGTCCTTAAAAATGAGCTATAACAAAGTCCAAATCATTGGGAAGGATACTTTCTACGGA
 CAGGTCCTTAAAAATGAGCTATAATAAAGTCCGAAAACCTCAGAAAGATACTTTTATGGC
 CAGGTCCTTAAAAATGAGCTATAACAAAGTCCAAATATTTGAGAAGGATACTTTGTATGGA
 ***** **

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 CTCGGGAGCTTGGTCCGGTTGCACCTGGATCACAAACATTTGAATTCATCAACCCCTGAG
 CTCAGGAGCTTGCACGATTGCACTGGACCAACAAATATTGAGTTTATAAACCAGAG
 CTCAGGAGCTTGAOCGGTTGCACCTGGATCACAAACATTTGAGTTTATCAACCCCGAG
 *** ***** **

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 GCGTTTATGGACTTACCTCGCTCCGCTTGGTACATTTAGAAGGAAACCGGCTCACAAAG
 GTTMTTATGGGCTCAACTTTCTCCGCTGGTGCATTTGGAAGGAAATCAGCTCACTAAG
 GCGTTTATGGACTTACCTCGCTCCGCTTGGTACATTTAGAAGGAAACCGGCTCACAAAG
 * ***** **

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 CTCCTCCAGACACATTGTCTCATTAAAGCTATCTCCAGATATTTAAACCTCTTTCATT
 CTCACCCAGATACATTGTCTCTTTGAGCTACCTCCAGATATTTAAATCTCTTTCATT
 CTCCTCCAGACACATTGTCTCTTTGAGCTATCTCCAGATATTTAAACCTCTTTCATT
 ***** **

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 AAGTACCTGTTCTGTCTGATAACTTCCT-GACCTCCCTCCCAAAGAAATGGTCTCCTA
 AAGTTCCTATACTGTCTGATAACTTCCT-GACCTCCCTCCCAAAGAGATGGTCTCCTA
 AAGNACCTGTACTGTATGATAACTTCATTGACCTCCCTCCCAAAGAAATGGTCTCCTC
 *** ** ***** *

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 CATGCCAAACCTAGAAAGCCTGTATTGCAATGGAAACCCATGGACCTGTGACTGCCATTT
 TATGCCATGACCTAGACGCTTACCTGCATGGAAACCCATGGACCTGTGATTGCCATTT
 TATGCCAAACCTAGAAAGCCTTACTTGCATGGAAACCCATGGACCTGTGACTGCCATTT
 ***** **

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 AAAGTGGTTGTCTGAGTGGATGCAGGGAACCCAGATATAATAAATGCAAGAAAGACAG
 AAAGTGGTTGTCTGACTGGATACAGGNNNNOCAGATGTAATAAATGCAAAAAGATAG
 AAAGTGGTTGTCCGAGTGGATGCAGGGAACCCAGGTA-ACTATCTTGT-TTGTGTTG
 ***** **

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 AAGCTCTTCAGTCTCAGCAATGTCCCT-TTGCATGAACCCAGGATCTCTAAAGGCA
 AAGTCCCTCTAGTCTCAGCTGCAGCTTCCACT-TTGCATGAACCCAGGATCTCTAAAGGCA
 TTTCTTTTTTATARKAGTATTTCTCAATTTCAATTTAGAATGATATCCCAAAGTC-
 * * * * *

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 GACCCCTTGGTATGTTACCATCTGGAGCTTCTATGTACAAAGCCACCATTTGATCCAT
 AGCCGTTAGCTATGTTCTCAGCTGCAGCTTCCAGTGTGCAAGCCACCATTTGACTCAT
 -CCCATACCTCCCCCCA-CTTCCTACCTACCATTC-CCATTTTGGC
 ** * *

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 CACTGAAGTCAAGAGCCTGGTTACTCAGGAGCAATGGATCTGCTCCCTCCACTCACCTC
 CCTGAAATCAAGAGCCTGACTATTCTGGAAGACAGTAGTTCTGCTTTCATCTCTCCCC
 CCTGGCATTCCCC-
 * * *

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 AAGATTTCATAGAACCTTTGGCTCCTTGTCTTTGAACATGACANANNTNTCTGGAATA
 AAGTTTCATGGCAACCTTTGGCTCCTCATTGAAATGACAGATCAGTCTGGAATG

rat_cDNA
 human_5+3_corrected
 mus_cDNA_5
 AGGCCGACATGGTCTGTAGTATCCAAAAGCCATCAAGGACATCACCAACTGCATTCACTG
 AAGCTAACATGGTCTGCAATATTCAAAAGCCCTCAAGGACATCACCATTTGCATTCACTG

rat_cDNA human_5+3_corrected mus_cDNA_5	AAGAAAATGACTACATCATGCTAAATGCGTCATTTTCCACAAATCTTGTGTGCAGTGTAG AAGAAAATGACTACATCGTGTAAATACTTCATTTTCAACATTTTGGTGTGCAACATAG -----
rat_cDNA human_5+3_corrected mus_cDNA_5	ATTATAATCACATCCAGCCAGTGTGGCACTTCTGGCTTTATACAGTGACTCTOCTCTGA ATTACGGTCACATTCAGCCAGTGTGGCAAATTTTGGCTTTGTACAGTGATTCTOCTCTGA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	TACTAGAAAGGAAGCCCCAGCTTACCGAGACTCCTTCACTGTCTTCTAGATATAAACAGG TACTAGAAAGGAGCCACTTGCTTAGTGAAACACCGCAGCTCTATTACAAATATAAACAGG -----
rat_cDNA human_5+3_corrected mus_cDNA_5	TGGCTCTTAGGCCCTGAAGACATTTTACCASCATAGAGGCTGATGTCAGAGCAGACCCCTT TGGCTCCTAAGCCTGAAGACATTTTACCAACATAGAGGCAGATCTCAGAGCAGATCCCT -----
rat_cDNA human_5+3_corrected mus_cDNA_5	TTTGGTTCACACAAGAAAAATTTCTTGCGAGCTGAACAGAACTGCCACCACACTTAGCA CTTGGTTAATGCAAGACCAAATTTCCCTTGCAGCTGAACAGAACTGCCACCACATTCAGTA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CATTACAGATCCAGTTTTCCTACTGATGCTCAAATCGCTTTACCAAGGGCGGAGATGAGAG CATTACAGATCCAGTACTCCAGTGAATGCTCAAATCACTTTACCAAGAGCAGAGATGAGGC -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CGGAGAGACTCAAATGGACCATGATCCTGATGATGAACATCCCAAAGTGGAAACGCACTG CAGTGAACACAAATGGACTATGATTTCAAGGGATAACAATACTAAGCTGGAACATACTG -----
rat_cDNA human_5+3_corrected mus_cDNA_5	TCTTGGTTGGCGGCACTATTGCCCCGAGCTGTCCAGGCAAGGGGACCCCTTCACTCACT TCTTGGTAGGTGGAACCGTTGGCCTGAAGTCCCAGGCCAAGGAGACCCCAACCCACAGC -----
rat_cDNA human_5+3_corrected mus_cDNA_5	TGGAATGGCTTCTAGCTGATGGGAGTAAAGTGAGAGCCCTTACGTTAGCGAGGATGGGC TGGATTGGCTTCTAGCTGATGGAAGTAAAGTGAGAGCCCTTATGTCAGTGAGGATGGAC -----
rat_cDNA human_5+3_corrected mus_cDNA_5	GAATCCTAATAGACAAAATGGGAAGTTGGAAGTGCAGATGGCTGACAGCTTTGATGCAG GGATCCTAATAGACAAAAGTGAAGTGGGAAGTGCAGATGGCTGATAGTTTTCACACAG -----
rat_cDNA human_5+3_corrected mus_cDNA_5	GTCTTTACCACTGCATAAGCACCAATGATGCAGATGCGGATGTTCTCACATACAGGATAA GCGTATATCACTGTATAGCAGCAATATGATGATGCAGATATTTCTACCTATAGGATAA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CTGTGGTAGAGCCCTATGGAGAAAGCACACATGACAGTGGAGTCCAGCACACAGTGGTTA CTGTGGTAGAACCTTTGGTTCGAAGCCTATCAGGAAAATGGGATTTCATCACACAGTTTTC -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CGGGTGAGAGCGCTGACCTTCCATGCTTTCCACGGGTGTTCCAGATGCTTCTATTAGCT TTGGTGAAACACTTGATCTTCATGCCATTTCTACTGGTATCCCAGATGCTTCTATTAGCT -----
rat_cDNA human_5+3_corrected mus_cDNA_5	GGATTCTTCCAGGGAACTGTGTTCTCTCGCCATCAAGAGACAGGCAAATCTTAACA GGGTTATTCCAGGAAACATGTGCTCTATCAGTCATCAAGAGACAGAAAGTTCTAACA -----

rat_cDNA human_5+3_corrected mus_cDNA_5	ATGGGACCTTAAGAATATTACAGGTACGCCAAAGATCAAGGTCATTACCAATGTGTGG ATGGCACATTAAGAATATTACAGGTACCCCCGAAAGACCAAGGTTATATCGCTGTGTGG -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CTGCCAACCCATCAGGGGCGGACTTTTCCAGTTTAAAGTTTCAGTTCAAAAGAAAGGCC CAGCCAACCCATCAGGGGTGATTTTGTATTTTCCAAGTTTCAGTCAAGATGAAGGAC -----
rat_cDNA human_5+3_corrected mus_cDNA_5	AAAGGATGGTTGACATGACAGGGAGGCAGGTGGATCTGGACTTGGAGAACCCAACTCCA AAAGGCCCTTGGAGCATGATGGAGAAACAGAGGGATCTGGACTTGATGAGTCCAATCCTA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	GTGTTTCCCTTAAGCAGCCAGCATCTTTGAAACTCTCTGCATCAGCTTTGACAGGGTCAG TTGCTCATCTTAAGGAGCCACAGGTGCACAACTCCGTACATCTGCTCTGATGGAGGCTG -----
rat_cDNA human_5+3_corrected mus_cDNA_5	AGGCTGGAAAACAAGTCTCCGGTGTACATAGGAAGAACAAACATAGAGACTTAATACATC AGGTTGGAAAACACACCTCAAGCACAACTAAGAGGCACAACTATCGGGAATTAACTCTCC -----
rat_cDNA human_5+3_corrected mus_cDNA_5	GGCGCGCTGGGGATTCCAGCTCCGGCGATTGAGGAGCATAGGAGGCAGCTCCCTCTCT AGCGAGCTGGAGATTCAACACATCGAGCTTTAGGGAGAAATAGGAGGCATTCCCTCCCT -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CTGCTCGGAGATTGACCCGCACTCTGGGCGAGCACTTCTAGAAAAGCCAAAAGAAATT CTGCTAGGAGAAATTGACCCACACATTGGGCGGCACTGTTGGAGAAAGCTAAAAGAAATG -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CTGTGCCAAAAAGCAAGAAATACCAAGTAAGCCAGTGCCACTGGCTGTTCCCTCTCG CTATGCCAGACAAGCGAGAAATACCAAGTGAGCCCAACCCCAAGTGGTCAACCAACTCC -----
rat_cDNA human_5+3_corrected mus_cDNA_5	TGGAACCTCACTGACGAGGAAAGGATGCCCTCTGGCATGATTCCCTCCAGATGAAGAAATCA CAAACATACCTGGTGAAGAAGACGATTCTCAGGCATGCTCGCTCTACATGAGGAATTTA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	TGGTTCTGAAAACCTAAGGCTTCTGGTGTCCAGGAAGGTCAACAACTGCTGACTCTGGAC TGGTCCCGCCACTAAGCTTTGAACCTTCCAGCAAGGACAGTGACTGCTGACTCCAGAA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CAGTAAATCATGGTTTTATGACGAGTATAGCTTCTGGCACAGAGTCTCAACTGTGAATC CAATATCTGATAGTCCATGACAAACATAAATTATGGCACAGAACTCTCCGTTGTGAATT -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CACAAACACTACAACTGAGCACCTTCCTGATTTCAAAATTATTTAGTGTAAACAAAGGTA CACAAATACTACCACCTGAAGAACCCACAGATTTCAAACTGTCTACTGTATTAATACTA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CAGCTGTGACAAAGAGTATGAACCATCCATAGCAAGCAAAATAGAAGATCAACCAACC CAGCATGTCAAGAAATATAAACCCCAACCATGTCAAGCCAAATACAGGCGCAACCAATC -----
rat_cDNA human_5+3_corrected mus_cDNA_5	AAAACCCAAATCATTATCTTTCCATC-----AGTAGCTGAAATTGAGATTCTG-CT AACATTCAATCCATGTCTTTCCACTGCTAATTGGAGCAACTGAATTTCAGGACTCTGACA -----

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CAGGCA---GGAAGAGCATCTTCCAAAGTGCAACCCCTGTAACAGGGGAAACATGGCT
GAGGGAAGAGGAAGAGAGCATTTCC--AGTA-ACCCCAATAACAGTAAGGACTATGATC

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACCTATGGCCATACCAACACATA--TAGTAGCTTTACCAGCAAAGCCAGTACAGTCTTGC
AAAGATGNTCAATGTCAAANATGCTTAGTAGCACCCACCAACAAA-CTATTA-----TTAG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

AGCCATAAATCCAACAGAAAGTTATGGACCTCAGATACCTATTACAGGAGTCAGCAGAC
AGTCAGTAAATACCACAAATAGTCAT-----CAGACATCTGTAGAGAGTGTAGTGAAC

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CTAGCAGTAGTGACATCTCTTCTCACACTACTGCAGACCCCTAGCTTCTCCAGTCACCCCT
CCAGGCACAATCACTTCTATTCTCACACTACTCAAATACTTAGCACCTCCACGTTCCCTT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CAGGTTCAACACACCCTGCGCTCTTTATTTACATTCCTAGAAACAACAATACAGGTA
CAGATCCACACACAGCTGCTCATTTCTCAGTTTCCGATCCCTAGANNNAATAGTACAGTTA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACTTCCCTTGTCTCAGGCACTTGGGAAGAGAGAGGACAATTTGGAGCAGAGGGAGAGTTA
ACATCCCGCTGTTCAGACGCTTTGGGAGGCAGAGGAAAATTGGCGAAGGGGGGGATTTA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

AAAACCCATAGAAACCCAGTTCTCCGACGGCATAGACACAGGACTGTGAGGCCAGCAA
TCAGCCCATATAGAACTCCAGTTCTGCGAOGGCATAGATACAGCATTTTCAGGTCAACAA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TCAGGGACCTGCTAACAAAAATGTGAGCCAAGTTCAGCCACAGAGTACCCTGGGATGT
CCAGAGGTTCTCTGAAAAAAGCACTACTGCAATTCTCAGCCACAGTGTCTCATGTGACAT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GCCACACATGTCTTCCGAGAGGGGCTCAGTGGCTACTGCAGCACTGTCACTTCCAA
GTCTGTCTGTCTTCCAGGAGAGGGCTCACCCTGCCACAGCAGCATTGTCTTTCCAA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GTTCAATCCCACTGCGCTCCCAAACTAATAATGTGGGGTCATAGCAGAAGAGTCTA
GTGCTGCTCCCATCACTTCCCAAGGCTGACATTGCTAGAGTCCCATCAGAAGTCTA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CCACGTGTGTCAAGAAACCACTGTACTATTTAAGGACAAACAAAATGTAGATATTGAGA
CAACTCTAGTCCAGATCCACTATTACTACTTGAGAACAAACCCAGTGTAGANNNGAAA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TAATAACAACCACTACAAAATATCCGGAGGGGAAAGTAACCAAGTGATTCTTACGGAAG
NNACACACCCACAATAAATATTCAGGACTNGAAATTTCCCAAGTGACTCCAACTGGTG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CAAGCATGACTTCTGTCCAACATCTGTATCCCTGGGGAAATCTCCTGTAGACAATAGTG
CAGTCATGACATATGCTCCACATCCATACCCATGGAAAAACTCACAAGTAACAGCCA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GTCACCTGAGCATGCTGGGAACATCCAAACTGGGAAAGATTCAAGTGAAACACACACCAC
GTTACCCACGTGTGTCTAGCAACCAATGAAGCTAAAAGAGATTCAAGTATTACATGCTCAC

rat_cDNA human 5+3 corrected mus_cDNA_5	TTCCAGGCCCCCTCAGCAGCCCTCAATACCA-----CAAGCACAATAATTCTCAAAGA TTTCAGGTGCTATCAGCAGCCCAATGACTATTATAGCCATTACAAGGTTTTCAAGAA -----
rat_cDNA human 5+3 corrected mus_cDNA_5	GGAAACTCCCTTGCCACCAGATCTTTGTAAATAACCAGAAGAGGGGGATGTTAAGA GGAAATTCCTGGCAACAGAACTTTGTAAATAACCATACCCAAAGGCAGATTAAAGA -----
rat_cDNA human 5+3 corrected mus_cDNA_5	ATCCATATCAATTGGTTTACAAAAGAACCCAGCCGCAAGCTTCCAAAATAGCTCCTC ATCAACATAAAGTTAGTTTACAAAAGCAGAGCTGTGATGCTTCTAAACATCTCCTG -----
rat_cDNA human 5+3 corrected mus_cDNA_5	TTTACCCACAG-GTCAGAGTTCCCCCTCAGATTCTACAACCTCTTTGACAAGTCCGCA CTTTACC-ACAGAGACAAAGTTCCCTTTCCATTTCACCACACTTTCAACAAGTGTGATG -----
rat_cDNA human 5+3 corrected mus_cDNA_5	CCAGCTCTGTCTACAACAATGGCTGCCACTCAGAACAGGGCAGTGAAGTAGTATCAGGT CAAATTCATCTAATACCTTGACTACGGCTCAGCAGCTACGACCAAA--ACACACAA-T -----
rat_cDNA human 5+3 corrected mus_cDNA_5	GCCAGAAGTCTCTCAGCAGGGAAGAAGCAGCCCTTCACCAAGTCTCTCCAG-TGCTTCC CCTGGAAGTCTTCCACAAAGAAGGAGCTTCCCTTC-CCACCCCTTAACCTATGCTTCC -----
rat_cDNA human 5+3 corrected mus_cDNA_5	TAGCACCATAAGCAGAGATCTAATACATTAACTTCTTGTCAACGGAAACCCCCACAGT TAGTATTATAAGCAAGAGACTCAAGTACAAAAGCATCTATCAACGCAACAGCAACCGC -----
rat_cDNA human 5+3 corrected mus_cDNA_5	GACAAGTCTACTGCTACTGCTATGTCTATTATGTCTGAAACCCACGAAACAGATCCAA AACAACTCTACTCTTCCCTGCATCTGTCTACTTATGAAACCCAAACAGAGAGATCTAG -----
rat_cDNA human 5+3 corrected mus_cDNA_5	AGAGCAGAAAGACCAATAAAGGGGCTCG--GAAGAACAGAAACACGCAACACCAC AGCACAACAATACAAAGAGAAGGACCTCAAGAGAAACAGGACTGACCCAAACATCTC -----
rat_cDNA human 5+3 corrected mus_cDNA_5	CCCCAGGCAGGTTTCTGGCTATAGTGCATACTCAGCTCTAACCAACAGCTGATACCCCCCT TCCAGACCAGAGTTCTGGCTTCACTACACCCACTGCTATGACNACCTCTTNGCTCTNNN -----
rat_cDNA human 5+3 corrected mus_cDNA_5	GGCTTTCAGTCAATCCCCACGACAGATGATGGTGGAAATGTAAGTGCAGTTGCTTATCA NGCATTCAGTCAATCCCCACGAAACACACTGGGATTTCAAGCACAATCAGTTTCA -----
rat_cDNA human 5+3 corrected mus_cDNA_5	CTCAACAACCTCTCTCTGGCCA---TAACTGAAGTGTGAG-AGTAC--ACCCAGAC TTCAAGAACTCTTAATCTGACAGATGTGATTGAAGAACTAGCCCAAGCAAGTACTACAC -----
rat_cDNA human 5+3 corrected mus_cDNA_5	TTTGGGAATACACAGCTTTGGAAACAACGTTGTTGAGCAATCACAGGAGAGTACCAC TTTGAAGAGCACAATGCTTCTGAAACAACTTTGTCCAGCAATCACACCAGAGTACCAC -----
rat_cDNA human 5+3 corrected mus_cDNA_5	AGTGAAGAGAGCTCA---GACAC---ACCAACCACTCCTCAGCAGTGGGGGCGCCCCC AACTAGGAAGAGCTCATTAGACACTCAACCAACCACTTCTTGAGCAGCAGTGTACTCT -----

rat_cDNA human_5+3_corrected mus_cDNA_5	AGTGCCTCACTCCCTTCCCCACCTCCTTTTACTAAGGGTGTGGTTACAGACAGCAAAGTCAC AATGCCAGTTCCCATCTCCCTCCCTTTACTCAGAGAGCAGTTACTGACAAAGTGGCGAC -----
rat_cDNA human_5+3_corrected mus_cDNA_5	ATCAGCTTTCAGATGACGTCAAATAGAGTGGTCACCATATATGAATCTTCAAGGCACAA TCCCATTTCCGGGCTTATGACAAATACAGTGGTCAAGCTGCAGGAATCCTCAAGGCACAA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	TACAGATCTGCAGCAACCTCAGCAGAGGCTAGCCCCAATCCTGAGATCATAACTGGAAC TCCNNNNNNNCA--AATGCCAAGTTCA-----CNAATTGNGAACNNNNNACTCNNNN -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CACTGACTCTCCCTCTAACTCTGTTTCCATCCACTTCTGTGCCAGCACTAAGGGTAGATTA NACTTCATCTACNTCTARTCTGTTACATTCTACTCCCATGCCAGCACTAACAACAGTTAA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	ACCACAGAATTCTAAATGGAAGCCCTCTCCTGGCCAGAACACAAATATCAGCTCAAGTC ATCACAGAATTCCAAATTAACTCCATCTCCTGGGCAGAAATACCAATTTTGGCAGAAACC -----
rat_cDNA human_5+3_corrected mus_cDNA_5	ATACTCCGAAACCRITGAGAAGGGCAAAAGGCCAGCAGTAAGCATGTCCCCCACCCTCAG ATACTCAGACATTGCTGAAAAGGCCAAAAGCCAGAAGTAAGCATGTTGGCT-ACTACAG -----
rat_cDNA human_5+3_corrected mus_cDNA_5	-CCTTCCAGAGGCCAGCACTCATGCCCTCACACTGGAATACACAGAAGCATGCAGAAAAGA GCTGTCCGAGGCCACCCTCTTGTTCAGATTGGGATGGACAGAGAACACAAAGAGAA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	GTGTTTTTGATAAGAAACCTGGTCAA-AAAC--CRACTTCCAAACATCTGCCTTACGTCT GTGACTTTGATAAGAAACCAGTTCAAGAAGCAACACTTCCAAACTCCTTCCCTTTGACT -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CTCTACCTTAAGACTCTATTGAAAAGCCAGAATAATTGGAGGAAAGGCTGCAGCTTTA CTTTGTCTAGGTATATATTGAAAAGCCAGATAGTTGGAGGAAAAGCTGCAAGTTTAA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CAGTCCAGCTAATTCAGACGTTTTTTCTTCTGAGGCTGTTGGAGACCCACTGCCCA CTATTCAGCTAATCAGATGCCCTTCTTCCCTGTGAAGCTGTTGGAAATCCCCTGCCCA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	TCATCCACTGGACCAGAGTTTCATCAGGANTTGAATATCCCAGGGACACAGAAAAGCC CCATTCAATTGGACCAGAGTNNNNTCAGGACTTGATTATCTAAGAGGAAACAGAAATAGCA -----
rat_cDNA human_5+3_corrected mus_cDNA_5	GGTTCACGTTGCTTCCCAATGGCACCTTGTCATCCAGAGGGTCAGTATTCAGGAACCTG GGGTCCAGGTTCTCCCCAATGGTACCTGTCCATCCAGAGGGTGGAAATTCAGGAACCGG -----
rat_cDNA human_5+3_corrected mus_cDNA_5	GACAGTACCTGTGCTCTGCATTTAATCCACTGGGCGTAGACCAATTTTCATGTCCTTGT GACAGTACTTGTGTTCCGCATCCAATCTGTTGGCAGACACCACTTCATGTCACCTTGT -----
rat_cDNA human_5+3_corrected mus_cDNA_5	CTGTGGTTTTTTTACCGGCAAGGATTTTGGACAGACATGTCAAGGAGATCAGTTTCACT CTGTGGTTTTCTATCCTCCAGGATCCTGGAGAGAGTACCAAAGAGATCAGTTTCACT -----

rat_cDNA human 5+3 corrected mus_cDNA_5	TTGGAAGTACTGTGGAACTAAAGTGCAGAGTGGAGGSTATGCCAGGCOCTACGGTTTCCT CCGGAAGCACTGTGGAACTGAAGTGCAGAGCAGAAGGTAGGCCAAGCCCTACAGTTAOCCT -----
rat_cDNA human 5+3 corrected mus_cDNA_5	GGATACTTGCATAACCAACGGTGGTCTCAGAAACGGCCAAAGGGAAGCAGAAAGGTCTGGG GGATTCTTGCAAAACCAACAGTTGTCTCAGAATCATCCAGGGGAAGTAGGCAGGCTGTGG -----
rat_cDNA human 5+3 corrected mus_cDNA_5	TACACCTGATGGAACATTGATCATCTATAATCTGAGTCTTTATGATCGTGGTTTTTACA TGACGGTTGACGGAACATTGGTCTCCACAACTCTAGTATTTATGACCGTGGCTTTTACA -----
rat_cDNA human 5+3 corrected mus_cDNA_5	AGTGTGTGGCCAGCAACCCATCTGSCCAGGATTCACTGTTGGTTAAGATACAAGTCATCA AATGTGTGGCCAGCAACCCAGGTGGCCAGGATTCACTGCTGGTTAAATACAGTCATTG -----
rat_cDNA human 5+3 corrected mus_cDNA_5	CAGCTCCCCCTGTCAATTATAGAGCAAAAGAGGCAAGCCATCGTTGGGGTTTTAGGTGGAA CAGCACCACTGTTATTTCTAGAGCAAGGAGGCAAGTCATTGTAGGCACCTTGGGGTGAAA -----
rat_cDNA human 5+3 corrected mus_cDNA_5	GTTTGAAACTGCCCTGCACCTGCAAAAGGAACTCCCCAGCCTAGTGTTCACCTGGGTCTTT GTTTAAAACTGCCCTGTACTGCAAAAGGAACTCCTCAGCCAGCGTTTACTGGGTCTCTCT -----
rat_cDNA human 5+3 corrected mus_cDNA_5	ATGATGGGACTGAACTAAAAACATTGCAGTTGACTCATTCCAGATTTTTCTTGATCCAA CTGATGGCACTGAAGTGAACCAATTACAGTTTACCAATTCAGTTGTTCTTATTTTCAA -----
rat_cDNA human 5+3 corrected mus_cDNA_5	ATGGAACCTCTGTATATAAGAAGCATCGCTCCTTCAGTGGGGGCACTTATGAGTGCATTG ATGGGACTTTGTATATAAGAAACCTAGCCTCTTCAGACAGGGGCACTTATGAATGCATTG -----
rat_cDNA human 5+3 corrected mus_cDNA_5	CCACAGCTCCTCAGGCTCAGAGAGAAGGGTAGTGATTCTTACTGTGGAAGAGGGAGAGA CTACCAGTTCCACTGGTTCGGAGCGAAGAGTAGTAATGCTTACAATGGAAGAGCGAGTGA -----
rat_cDNA human 5+3 corrected mus_cDNA_5	CAATCCCCAGGATAGAACTGCOCTCTCAGAAATGGACTGAGGTGAATTTGGGTGAGAAAT CCAGCCCCAGGATAGAACTGCAATCCAGAAAGGACTGAAGTGAATTTGGGGACAAAT -----
rat_cDNA human 5+3 corrected mus_cDNA_5	TACTACTGAACTGCTCAGCTACTGGGGATCCAAAGCCTAGAATAATCTGGAGCTGCCAT TACTACTGAACTGCTCAGCCACTGGGGAGCCCAACCCCAATATGTGGAGGTTACCAT -----
rat_cDNA human 5+3 corrected mus_cDNA_5	CCAGGGCTGTCTCGACCACTGGCAAGAAATGGGCAAGCCGAATCCAGCTCTACCCAAATG CCAGGGCTGTGTCTCGACCACTGG-----GCAGCTGGATCCAGCTCTACCCAAATG -----
rat_cDNA human 5+3 corrected mus_cDNA_5	GATCCTTGGTGGTTGGGTCACTGACGGAAAAAGACGCTGGTGACTACTTATGTGTGGCAA GATCCCTGTTTATTGTGATCAGTAACAGAAAAAGACAGTGGTGTCTACTTGTGTGTGGCAA -----
rat_cDNA human 5+3 corrected mus_cDNA_5	GAAACAAAAATGGGAGATGACCTAGTCTGTATGCATGTCCGCCTGAGATTGACACCTGCCA GAAACAAAAATGGGGGATGATCTGATACGTGATGCATGTAGCCTAAGACTGAAACCTGCCA -----

rat_cDNA
human_5+3_corrected
mus_cDNA_5

AAATTGAACAGAAGCAGTATTTTAAAGCAAGTGCTCCATGGGAAAGATTTCCAACTTG
AAATTGACCACAGCAGTATTTAGAAAGCAAGTGCTCCATGGGAAAGATTTCCAACTAG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACTGCAAGGCTCTGGCTCCCCGTGCTGAGGTATCTGGAGTTTGCTGATGGGACAG
ATTGCAAGCTTCGGGCTCCCGAGTCCAGAGATATCTGGAGTTTGCTGATGGGAACCA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TGCTCAACAATGTAGCCCAAGCTGATGACAGTGGCTATAGGACCAAGAGGTACACCTTT
TGATCAACAATGCAATGCAAGCCGATGACAGTGGCCACAGGACTAGGAGATATACCTTT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TCCACAATGGAACTTGTATTTCAACAAGCTTGGGATGGCAGAGGAAGGAGATTATATCT
TCAACAATGGAACTTTATCTTCAACAAGTTGGGGTAGCGGAGGAAGGAGATTATACTT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GCTCTGCCAGAACACCTTAGGGAAGATGAGATGAATGTCCACCTAACAGTTCTAACAG
GCTATGCCAGAACACCTTAGGGAAGATGAATGAAGGTCCACTTAACAGTTATAACAG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CCATCCACGGATAAGGCAAGCTACAGACCCCATGAGGCTCAGGGCTGGAGAACAG
CTGCTCCCCGATTAAGGCAGAGTAACAAACCAACAGAGAAATCAAGCTGGAGACACAG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CTGTCTTGACTGCGAGGTCCTGGGGAACCGAAGCCCAATGTATTTTGGTTGCTGCCTT
CTGTCTTGACTGTGAGGTCCTGGGATCCCAACCAAAATATTTTGGTTGCTGCCTT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CCAACAATGTCAATTCATTTCTCCAATGACAGGTTCAATTTCTGCAATAGACTTTGT
CCAATGACATGATTTCTTCTCCATGTATAGGTACACATTTCTGCAATGGGCTTTGA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CCATCCATAAAGTGAACCACTTGACTCTGGGGACTATGTGTGCGTAGCTCAGAATCCTA
CCATCAACAAGTGAACCTGCTCGATTTCTGGAGAGTACGTATGTGTAGCCCGAATCCCA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GTGGGGATGACACTAAGACATACAACTGGAATTTGCTCTAAACCTCCATTAACTAATG
GTGGGGATGACACCAAAATGTACAACTGGATGTGGTCTCTAAACCTCCATTAACTAATG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GCCTGTATGCAACAAGACTGTTATTAAGCCACAGCATTCGGCACTCCAAAAATACT
GTCTGTATACAAACAGAACTGTTATTAAGCCACAGCTGTGAGACATTCCAAAAACACT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TTGACTGCAGAGCAGATGGGATCCCATCTTCCAGGTCAGTGGATTATGCCAGGCAATA
TTGACTGCAGAGCTGAAGGGACCAATCTCTGAACTCATGTGGATCATGCCAGGCAATA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TTTTCCTGCCAGCTCCATACTTTGGAAGCAGAGTCAGGTCATCCAAATGGAACTTGG
TTTTCCTCACAGCCCCATCTATGGAAGCAGAAATCACAGTCCATAAAATGGAACTTGG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

AGATGAGGAACATCCGCTTTCTGACTCTGCGGACTTCACCTGTGTGGTTCCGAGCGAGG
AAATTAGGAATGTGAGGCTTTCAATTCAGCCGACTTTATCTGTGTGGCCCGAATGAAG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GAGGAGAGAGTGTGTTGGTAGTGCAGTTAGAAGTCTAGAAATGCTGAGAAGACCAACAT
GTGGAGAGAGCGTGTGTTAGTACAGTTAGAAGTACTGGAAATGCTGAGAAGACCGACAT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TCAGAAACCCATTCAACGAAAAAGTCATCGCCCAAGCTGGCAAGCCCGTAGCACTGAAC
TTAGAAATCCATTTAATGAAAAATAGTTGCCAGCTGGGAAAGTCCACAGCATTGAATT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GCTCTGTGGATGGGAACCCGCCACCTGAAATTACCTGGATCTTACCTGAOGGCACACAGT
GCTCTGTGATGGTAACCCACCACTGAAATAATCTGGATTTTACCAATGGCACACGAT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TTGCTAACAGACACACAATTCCCGTATCTGATGGCAGGCAATGGCTCTCTCATCCTTT
TTTCCAATGGACCAAAAGTTATCAGTATCTGATAGCAAGCAATGGTTCTTTTATCATT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACAAAGCAACTCGGAACAAGTCAGGGAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGCT
CTAAACAACCTCGGAGGATGCAGGAAAAATATCGCTGTGCAGCTAGGAATAAAGTTGGCT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACATCGAGAACTCATCTGTAGAGATTGGGCAGAAGCCAGTCATTCTGACATAAGAAC
ATATTGAGAAATTAGTCATATTAGAAATTGGCCAGAAGCCAGTTATTCTTACCTATGCAC

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CAGGGATGGTGRAGAGCGTCAGTGGGGAACCGTTATCACTGCATTGTGTCTGATGGGA
CAGGGACAGTAAAGGCATCAGTGGAGAATCTCTATCACTGCATTGTGTCTGATGGAA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TCCCCAGCCAAATGTCAAGTGGACTACACCGGGTGGCCATGTAATCGACAGGCTCAAG
TCCCTAAGCCAAATATCAATGGACTATGCCAAGTGGTTATGTAGTAGACAGGCTCAAA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TGGATGGAAATACATACTGCATGAAATGGCAGCTGGTCATCAAAGCAACACAGCTC
TTAATGGGAATACATATTGCATGACAAATGGCACCTTAGTCATTAAAGAACCAACAGCTT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACGACCAAGGAAATATATCTGTAGGGCTCAAAACAGTGTGGCCAGGCAGTTATTAGCG
ATGACAGAGGAACTATATCTGTAAAGGCTCAAATAGTGTGGTCATACACTGATTACTG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TGTCAGTGTGTTGTGGCTACCTCCCGAATCATAAACTACCTACCCAGGAACATGC
TTCCAGTAATGATTGTAGCTACCTCCCGAATTACAAATGCTCCACCCAGGAGTATTG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TCAGGAGGACAGGGGAAGCCATGCAGCTCCACTGTGTGGCCTTGGGAATCCCCAAGCCAA
TCACCAGGACAGGGGAGGCTTTGAGCTCCACTGTGTGGCCTTGGGAGTTCCCAAGCCAG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

AAGTCACCTGGGAGACGCAAGACACTCCCTGCTCTCAAAGCAACAGCAAGAAACCC
AAATCAGATGGGAGATGCCTGACCACTCCCTTCTCTCAACGGCAAGTAAGAGAGGACAC

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ATAGAAGTGAGATGCTTACCCACAAGGTACGCTGGTCATTGAGATCTCCAAACCTCGG
ATGGAAGTGAGCAGCTTCACTACAGGTACCTTAGTCATTGAGATCCCCAAACCTCGG

rat_cDNA
human_5+3 corrected
mus_cDNA_5

ATTCCGGAGTCTATAAGTGCAGAGCTCAGAACCTACTTGGGACTGATTACGCAACAACCTT
ATTCTGGGATATACAAATGCACAGCAAAGAACCCACTTGGTAGTGATTATGCAGCAACGT

rat_cDNA
human_5+3 corrected
mus_cDNA_5

ACATCCAGGTAAGTCTGACAGGAGGGGGAGACTTAAATTCACAGAGTCCACATCCACA
ATATTCAAGTAATCTGACATGAA----ATAATAAGT-CAACAA----CATCTGGGCA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

GGGTTTATTTTTTGGAGAGAGTTTAAATCAAAGGCAGCCATAGGCATGTAAATGAGTCTGA
GAATTTATTTTTTGGAGAGAGTTTAAATCAAAGGCAGCCATAGGCATGTAAATGAATTTGA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

ATACATTTACAGTATTAAATTTACAATGGACATGCGA--TGA---GACTTGTAAATGAAA
ATACATTTACAGTATTAAATTTACAATGAACATGCAAAATAAAAGGACTTGTAAATRAAT

rat_cDNA
human_5+3 corrected
mus_cDNA_5

GCATTGTGAAGTGAA---ACCGAGTCTCTG--TGGATCTCAAAGCAAACCTCTTAACCTTAA
GCATTATGAAGTGATGACTGATTTATTTAATGGATCTCAAACCAAACCTTTTAACCTTAA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

GGCACTTTGATTTTGGCAACAAATATAACAAACATTAAGAGAAAAAATGATCCACTAC
GGCACTTTTATTTTGGCAACAAATAACAATAAACAA---ACATTGAAACGGTTCACATAT

rat_cDNA
human_5+3 corrected
mus_cDNA_5

GAAATAACAAACGGCTAATGCACCTGAATTCT-CAGTAAAAAGACCTTTCTCTGCTAAC
AAAATAACAAATGGCTAATGTACCTGAATTTTTTCACTAAAAAAA---TGAACCTT-CTAAT

rat_cDNA
human_5+3 corrected
mus_cDNA_5

AGTTGCCAGCTGCCTCGTGTCTGTTTCCACCAATGTCACAAACATCGCACACAGGGTGA
A---CCAGTTGCCTAGTGTCCACCTCCTATCAATGTTACAAGCATGGCACTCAG---A

rat_cDNA
human_5+3 corrected
mus_cDNA_5

ATGGAGTCAACGGGAAGATTAAAGTTTGCAGTCTGTGTAATCTCAATGTACAAATATTC
ACAGAGCAATGGAAAAATTAATCTGC-----AATCT--ATGTATAAATATTT

rat_cDNA
human_5+3 corrected
mus_cDNA_5

TGTCNCTGGTTTATAAATTTT-GATAAAACCGAAAAAATAAATAAATAAATAAATAAATAA
TGT---GGTTTATAAATTTTTTGTCTAAACCTACAGAAATAAG-----

rat_cDNA
human_5+3 corrected
mus_cDNA_5

AAAA

(rat_cDNA: SEQ ID NO:7)

(human_5+3 corrected: SEQ ID NO:8)

(mus_cDNA_5: SEQ ID NO:9)

Figure 15

rat	MQVRGREVSGLLISLTAVCLVVPFSGRACPRRCACYVPTVEHCTFRYLTSIPDGIPANVE
human_5+3_corrected	MKVKGRTGICLLVSEFAVICLVATPGGKACPRRCACYMPTVEHCTFRYLTSIPDSIPPNVE
mouse_5_corrected	MQKRGREVSCLLISLTAVCLVVPFSGRVCFPRRCACYVPTVEHCTFRDLTSIPD-GPANVE
rat	RINLGYNSLTRLTENDFDGLSKLELIMLHSHNGIHRVSDKTFSGLSLQVLKMSYNKVQII
human_5+3_corrected	RINLGYNSLVRIMETDFSGLTKELELIMLHSHNGIHTIPDKTFSDLQALQVLKMSYNKVRL
mouse_5_corrected	RVNLYNSLTRLTENDFDGLSKLELIMLHSHNGIHRVSDKTFSGLSLQVLKMSYNKVQII
rat	RKDTFFYGLGSLVRLHLDHNNIEFINPEAFYGLTSLRLVHLEGNRLTKLHPDFTVSLSYLQ
human_5+3_corrected	QKDTFFYGLRSLTRLMDHNNIEFINPEVFGINFLRLVHLEGNQLTKLHPDFTVSLSYLQ
mouse_5_corrected	EKDTLYGLRSLTRLHLDHNNIEFINPEAFYGLTLLRLVHLEGNRLTKLHPDFTVSLSYLQ
rat	IFKTSFIKYLFLSDNFLTSLPKEMVSYMPNLESYLHGNPWTCDCHLKNLSEWMOGNPDI
human_5+3_corrected	IFKISFIKFLYLSNFLTSLPKQEMVSYMPDLDSLYLHGNPWTCDCHLKNLSDWIQ--PDV
mouse_5_corrected	IFKTSFIKXYLYDNF-TSLPKEMVSSMPNLESYLHGNPWTCDCHLKNLSEWMOGNP--
rat	IKCKKDRSSSSPQOCPLCMNPRIKGRPFAMVPSGAFLCTKPTIDPSLKSKSLVTOEDNG
human_5+3_corrected	IKCKKDRSPSSAQOCPLCMNPRTSKGKPLAMVSAAFQCAKPTIDSGLKSKSLTILEDSS
mouse_5_corrected	-----
rat	SASTSPQDFIEPFGSLSLNMTXSGNKADMVCSIQKPSRTSPTAFTEENDYIMNASFST
human_5+3_corrected	SAFISPGGFMAFPFGLTLMNTDQSGNEANMVCSIQKPSRTSPTAFTEENDYIVLNTSFST
mouse_5_corrected	-----
rat	NLVCSVDYNHIQPVWQLALYSDSPLILERKQILTETPSLSRYKQVALRPEDIFTSIEA
human_5+3_corrected	FLVCNIDYGHQIPVWQILALYSDSPLILERSHLLSETPQLYKYKQVAPKPEDIFTNIEA
mouse_5_corrected	-----
rat	DVRADPFWFQEQKIVLQINRTATTLSTLQIQFSTDAQIALPRAEMRAERLKWIMILMNN
human_5+3_corrected	DLRADPSWLMQDQISLQINRTATTLSTLQIQYSSDAQITLPRAEMLPVKHKWTMISDNN
mouse_5_corrected	-----
rat	PKLERTVLVGSTIALSCPGKGDPSPHLENLLADGSKVRAPYVSEDGRILIDKNGKLELQ
human_5+3_corrected	TKLEHTVLVGSTVGLNCPGQGDPTPHVWLLADGSKVRAPYVSEDGRILIDKSGKLELQ
mouse_5_corrected	-----
rat	ADSEFDAGLYHCISTNDADADVLTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTGV
human_5+3_corrected	ADSEDTGVYHCISSNYDDADILTYRITVVEPLVEAYOENGIHTVFIGETLDLPCHSTGI
mouse_5_corrected	-----
rat	PDASISWILPGNTVFSQPSRDRQILANGTLRILQVTPKQOGHYQCVANPFGADFSSTKV
human_5+3_corrected	PDASISWVIFGNVLYQSSRDKKVLNNGTLRILQVTPKQOGYYRCVANPFGVDLIFQV
mouse_5_corrected	-----
rat	SVQKKGQRMVEHDREAGGSGLGEPNSSVSLKQFASLKLASALTGSEAGQVSGVHRKNK
human_5+3_corrected	SVRMKGQRPLEHDGETEGSGGLDESNPFAHLKEPPGAQLRTSALMEAEVGHSTSTSKRH
mouse_5_corrected	-----
rat	HRDLIHRRGDSTLRREFREHRRQLPLSARRIDPQWAAALLEKAKKNKSVPAKQENTTVKPV
human_5+3_corrected	YRELTQRRGDSTHRRFFRNRHFPSPARRIDPQWAAALLEKAKKNAMPKRENTTVSPP
mouse_5_corrected	-----

rat	PLAVPLVELTDEEKDASGMIPDEEFMVLTKASGVPGRSPTADSGPVNHGFMSTIASGT
human_5+3_corrected	PVVTQLFNIPGEEEDSSGMLALHEEFMVPATKALNLPARTVTADSRITSDSPMTNINYGT
mouse_5_corrected	-----
rat	EVS-TVNPQTLQSEHLPDFKLFSVINGTAVTKSMNPSIASKIEDTTNQNPIIIFP---SV
human_5+3_corrected	EFSPVVNSQILPPEEPTDFKLSTAIKTTAMSKNINPTMSSQIQGTTNQHSSSTVPILLGA
mouse_5_corrected	-----
rat	AEIRDSAQAGRAS--SQSARPVTCGMATYGHNTYSSFTSKASTVLQPINPTESYGPQI
human_5+3_corrected	TEFQSDOMGRGREHFQSRPPIITVMTIKOVNVKMLSSTTNKL--LLESVNTTNSH--QT
mouse_5_corrected	-----
rat	PITGVSRPSSSDISSHTTADPSFSSEHPSGSHTTASSLEHIPPNNNTGNFPLSRHLGRERT
human_5+3_corrected	SVREVSEPRNHFYSHTTQILSTSTFSPDFHTAHSQFPPIRNS-TVNIPLFRFRGRQRK
mouse_5_corrected	-----
rat	IWSRGVKNPHRTPVLRHRHRTVVPALKGPANKNVSQVPATEYPMCHTCPSAEGTLVA
human_5+3_corrected	IGGRGRIISPYRTPVLRHRHYSIFRSTTRGSSEKSTTAFSATVLNVTCLSLPRERLTTA
mouse_5_corrected	-----
rat	TAALSVPSSSHSALPKTNVGVIAEESTTVVKKPLLEKDRQNVDBIITTTTKYSGGES
human_5+3_corrected	TAALSFPAAPIITFPKADIARVPSEESTTLVQNPLLLLENKE--SVEKTPTTIKYFRTBI
mouse_5_corrected	-----
rat	NHVIPTASMTSAPTSVSLGKSPVDNSGHLSPGTTIQTKDSVETTPLPSPPLSTP--SIP
human_5+3_corrected	SQVTPPGAVMTYAPTSIPMEKTHKVNASYPRVSSSTNEAKRDSVITSSLSGAIITKPMITII
mouse_5_corrected	-----
rat	TSTKFSKRKTPELHQIFVNNQKKEGMLKNFYQFGLQKNPAKLPKIAPELLPTGQSSPSDST
human_5+3_corrected	AITRFSRRKIIPWQNEFVNNHNPFGRLRNQHKVSLQKSTAVMLPKTSPALPQROSSPFHT
mouse_5_corrected	-----
rat	TILTSFPFALSTTMAATONKGTVEVVGARSLSAGKQ-PFTNSSPVLPSITIKRSNTLNF
human_5+3_corrected	TILTSVMQIPSENTLTATHTTTKTHNPG-SLPT-KKELPFPPLNPMPLPSIISKDSSTKSI
mouse_5_corrected	-----
rat	ISTETPT-VTSPTATASVIMSETQRTSKEAKDQIKG-P-RKNRNNANTTPROVSGYSAY
human_5+3_corrected	ISTQTAIPATPTTFASVITYETQTERSRAQTIQEQEPQKNRTDPNISPDQSSGFTTF
mouse_5_corrected	-----
rat	SALTADTPLAFSHSPRODDGNGVSAVAYESTTS--LLAITELFEKYTQTLGNTTALETT
human_5+3_corrected	TAMTP--PALAFTHSPPENTTGISSTISFHSRTILNLTDVIEELAQASTQTLKSTIASETT
mouse_5_corrected	-----
rat	LLSKSQESTTVKRAS-DTP-FPLLSSGAPFVPTSPPPFTKGVVTDKVTSAFQMTSNRV
human_5+3_corrected	LSSKSHQSTTRKASLDTPFIPFLSSSATIMPVPISEFFTQRAVTITRGDSHFRLNTTV
mouse_5_corrected	-----
rat	VTIYESSRHNTLQQPSAEASPNPEIITGTTDSPSNLFFSTSVPAIRVDKPNKSKWKPSF
human_5+3_corrected	VKLHESSRHN-LQMPSSOLEP-----LTSSTSNLLHSTPMPALTTVKSQNSKLTSPSP
mouse_5_corrected	-----
rat	WFEHKYQLKSYSETIERGKRPAVSMSPHLSLPEASTHASHWNTQKHASKSVFDKKPGQNP
human_5+3_corrected	WAEQFWHKPYSDIAEKGGKFEVSMLATTGLSEATTIVSDWDGQKNTKKSDFDKKPVQEA
mouse_5_corrected	-----

rat -TSKHLPPYVSLPKTLLKKPRIIGGKAASFTVPANSDVFLPCEAVGDLPIIHWTRVSSGX
human_5+3_corrected TTSKLLPFDLSRYIFEKPRIVGGKAASFTIPANSDAFLPCEAVGNPLPTIHWTRVS-GL
mouse_5_corrected -----

rat EISQGTQKSRFHVLPNGTLSIQRVSIQDRGQYLCSAFNPLGVDHFFVLSVVFYPARILD
human_5+3_corrected DLSRGNQNSRVQVLPNGTLSIQRVSIQDRGQYLCASNLFGTDHLHVLSVVSYPRIILE
mouse_5_corrected -----

rat RHVKEITVHFGSTVELKCRVEGMPRETIVSWILANQTVVSETAKGSRKVVVTPDGTLLIYN
human_5+3_corrected RRTKEITVHSGSTVELKCRAEGRPSFTVTWILANQTVVSESSQGSROAVTVTDGTLVLHN
mouse_5_corrected -----

rat LSLYDRGFYKCVASNPSSQDSSLVVKIQVITAPPVITEQKROAIVGVLGSSLKLPTAKGT
human_5+3_corrected LSIYDRGFYKCVASNPSSQDSSLVVKIQVIAAPPVILEQRRQVIVGTWGESLKLPTAKGT
mouse_5_corrected -----

rat PQPSVHWVLYDGTTELKPLQLTHSRFFLYPMGTLYIRSIAPSVRGTYECIATSSSGSERRV
human_5+3_corrected PQPSVHWVLYDGTTEVKELQFTNSKLLFLSNGTLYIRNLASSDRGTYECIATSSSGSERRV
mouse_5_corrected -----

rat VILTVEEGETIPRIETASQWTEVNLGEKLLLNCSATGDFKPRIIWRLPKAVIDQWHRM
human_5+3_corrected VMLTMEERVTSPIEASQKRTVNFQDKLLLNCSATGEPKQIMWRLPSKAVVDQ-----
mouse_5_corrected -----

rat GSRHIVYPNGSLVVGSVTEKDAGDYLCVARNKMGDDLVMHVLRILTPAKIEQKQYTKKQ
human_5+3_corrected GSWIHVYPNGSLFIGSVTEKDSGVYLCVARNKMGDDLVMHVSLRLKPAKIDHKQYFRKQ
mouse_5_corrected -----

rat VLHGKDFQVDCRASGSPVPEVSWSLPDGTVLNNVAQADDSGYRTKRYTLFHNGTLYFNKV
human_5+3_corrected VLHGKDFQVDCRASGSPVPEISWSLPGDTNINNVAQADDSGHRTRRYTLFNNGTLYFNKV
mouse_5_corrected -----

rat GMAEEGDYICSAQNTLGKDEMKVHLTVLTAIPRIQSYKTMRLRAGETAVIDCEVTGEF
human_5+3_corrected GVAEEGDYTCYAQNTLGKDEMKVHLTVITAAPRIQSNKTNKRIKAGDTAVIDCEVTGDF
mouse_5_corrected -----

rat KPNVFWLLPSNNVISFSNDRFTFRANRLSIHKVKPLDSGDYVCVAQNPSGDDTKYKLD
human_5+3_corrected KPKIFWLLPSNDMISFSIDRYTFHANGSLTINKVKLLDSGEYVCVARNPSGDDTKMYKLD
mouse_5_corrected -----

rat IVSKPPLINGLYANKTVIKATAIRHSKRYFDCRADGIPSSQVTWIMPGNIFLPAPYFGSR
human_5+3_corrected VVSKPPLINGLYTNRTVIKATAVRHSKXHFDCRAEGTPSPEVMWIMPDNIFLTAPYFGSR
mouse_5_corrected -----

rat VTVHPNGTLEMRNIRLSDSADFTCVVRSEGGESVLVQLEVLEMLRRPTFRNPFNEKIVA
human_5+3_corrected ITVHKNGTLEIRNVRLSDSADFTCVARNEGGESVLVQLEVLEMLRRPTFRNPFNEKIVA
mouse_5_corrected -----

rat QAGKPVALNCSVDGNPPPEITWILPDGTQFANRPHPNSPYTMAGNGSLILYKATRNKSGKY
human_5+3_corrected QLGSXTALNCSVDGNPPPEIIWILPENGTRFSNGPQSYQYLIASNGSFTIISKTTREDAGKY
mouse_5_corrected -----

rat RCAARNKVGYTEKLILLEIGQKPVILTYEPGMVKSVSSEPLSLHCVSDGIPKPNVKWTTP
human_5+3_corrected RCAARNKVGYTEKLVILEIGQKPVILTYAPGTVKGLSGBSLSLHCVSDGIPKPNIKWTMP
mouse_5_corrected -----

```

rat          LVIQNLQTSDSGVYKCRQNLGLTDYATTYIQV
human_5+3_corrected LVIQNPQTSDSGIYKCTAKNPLGSDYAATTYIQV
mouse_5_corrected -----

```

(rat: SEQ ID NO:10)
(human_5+3_corrected: SEQ ID NO:11)
(mouse_5_corrected: SEQ ID NO:12)

•

[illegible]

PITGYSRPSSSDISHTTADPSFSSHPGSGHTTASSLFHPIPRNNNTGNFPLSRHLGREERT
SVREVSEPRHNHFYSHTTQILSTSTFSPDEHTAAHSQFFIPRNS-TVNIFLFRFRGRQRK
., **,* ..: **** * *,. :. **,* * * ****, * :.* * :.*.*.

INSRGEVKNPHRI FVLRRHRHTVRPAIKGFANKNVSOVPATEYPMCHTCPSAEGLTVA
TGGRGRIISPYRTFVLRRHRYSLFRSTTRGSSEKSTAFSATVLNVTCLSCLPRERLTTA
* : * * * : * : * * * * * : * : * : * : * : * * * * : * : * * * *

TAALSVPSSSHSALPRTNNVGVIAEESTTVVKKPLLLFKDKQNVDIRIITTTTKYSGGES
TAALSFPSPAAPITFPKADIARVPSEESTTLVONPLLLLENKP--SVEKTPPTIKYFRTEI
***** *: : : : : * :***** : : : : : * : : * * * *

NHVIPTEASMTSAFTSVSLGKSPVDNSGHLSMPGTIQTGKDSVETTFPLPSPLSTP--SIP
SQVPTPGAVMTYAPTSLPMETHKNVNASYPVRSSTNEAKRDSVITSSLSGAITKPENTII
. * * * * * : : * : : . * : : * * * : * * *

TSSTKFSKRKTPLHQIFVNNQKKEGMLKNPYQFGLQKNPAAKLPKTAIPLPTGQSSPSDST
AITRFSRRKIPWQQNFVNNHNPGRILRNQHKVSLQKSTAVMLPRTISPALPQRQSSPFHFT
: * : * : * * * : : * : * : : : * : * : * : * : * : * : * : *

TLLTSPPFALSTTMAATONKGTVEVSGARLSAGKQPFNTSSPVLFTSTIKRSNTLNL
TILSTSMQIPSNLTILTAHHTTKTTPNG-SLPTKKELPPFPLNPLMPSIISKDSSTKSII
** ** * *:::..: *:::..: ** :. **: *:::*** ** * *::

STETPT-VTSPTATASVIMSETQRTSRKEAKDQING-P-RKNRMNANTTPRQVSGYSAYS
STQTAIPATPTTFFPASVITYETQTERSRACTIONREQEPQKNRTDPNISFDQSSGFTTPT
.*. :*. ***** ** * : * : * :***. :.* :* * **:: :

ALTTADTFLAFSHSPRODDGNNVSAYAYHSTTS--LLAITELFEKYTQTLGNTTALETTL
AMT'P--PALAPHTSPPENTTGISSTISFHSRTLNLTDVIEELAQASTQTLKSTIASETTL
.. .***:*** :: * *:::** * . * ** : **** * * ****

LSKSQESTTVKRAS-DTP-FPLLSGAPPVPTSPPPPTKGVVTSKVI8AFQMTSNRVV
SEKSHQSTTTTKASLDTPFPLFSSSATLMEVPISPPPTQRAVTDTRGDSHFLMTNTVV
..:** ***:*** *.*.****.***.:***:** **

TIYESRRHNTDLQPPSAEASPNPEIITGTDTDSPNLFPSTVSPALRVDEPQNSKWKPSFW
 KIHESRRHN--LQMPSSQLEF-----LTSTSNLLHSTPMPALTIVKSSQNSKLTPSFW
 :***** ***: * * * * * : * * * * * : * * * * * : * * * * *

PEHKYQLKSYSETIEKGKRPAVSMSPHLSLPEASTEASHWNTQKHAEKSVFDKPGQN-
AEYQFWHKPYS DIAEGKKFEVSMLATTGLSEATTLVSDWDGQIKTKKSDFDKPVQEAT
*: : * : : * : : * : : * : : * : : * : : * : : * : : *

```

TSKHLPVYSLPKILLKKPRIIGGKAASFTVPANSDFVLPCEAVGDPLPIHWTRVSSGXE
TSKLLPFDLSRYLFEKPRIVGGKAASFTIPANSDFLPCAVGNPLPIHWTRVGS-GLD
** *: * : :*****:*****:*****:*****:*****:*****:

```

ISQGTQKSRFHVLPNGTLSIQRVSIQDRGQYLCSAFNPLGVDDHFVSLSVVFYPARILDR
LBRGNNSRQVQLPENGTLTIQRVEIQDRGQYLCASNLFQTDHLVLTLSVVSYPPRIER

HVKEITVHFGSTVELKCRVEGMPRPVTVSWILANQTVV6SETAKGSRKVVWVFPDGLTLIIYNL
 RTKEITVHSGSTVELKCRAGEGRPSPTVTVWILANQTVV6SSQGSROAVTVDPDGLVLHNL
 : ***** . * * * * * ***** : ; * * : * * * * : * *

SILYDRGFYKCVASNPSSGQDSLIVKIQVITAPPVILEQRQAIVGVGLGSCLKLPCTAKGTFF
SITYDRGFYKCVASNPSSGQDSLIVKIQVIAAPPVILEQRQQVITVGWGESLCLKPCTAKGTFF
*****+*****+*****+*****+*****

QPSVHWVLYDGTTELKPLQLTSHRFFLYPNGLTYIRSIAPSVRGTYECIATSSSGSERRVV
QPSVYVNLSDGTEVVKPLQFTNSKLFLEFNGTLYIRNLASSDRGTYECIATSSSGSERRVV
***** **

```
ILTVEEGETIPRIETASQKRWTEVNLGKLLINC SATGDPKFRIINRLPSKAVIDQNHRMG  
MLTMEERVTSPIREAASQKRTEVNFGDKLLINC SATGEKPQLIWRLP SKAVVDQ-----G  
*:~:* * ~~~~:*** ~~~~~:*****~::~*****~* *
```

```

rat      SRIHVYPNGSLVVGSVTEKDGXYLCVARNKMGDDLVLMHVRLRLTPAKIEQKQYFKQV
human_5+3_corrected SWIHVYPNGSLFIGSVTERKSGVYLCVARNKMGDDLVLMHVSLRLKPAKIDHKQYFRQV
* *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

rat      LHGKDFQVDCASGSPVFEVSWSLPDGTVLNNVAQADDSGYRTKRYTLFENGTLYFNNVG
human_5+3_corrected LHGKDFQVDCASGSPVFEISWSLPGDTMINNAMQADDSGHRTRRYTLFNNGTLYFNKVG
*****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

rat      MAEGDYICSAQNTLGKDEMKVHLTVLTAIPRIQSYKTMRLRAGETAVLDCSEVTGEPK
human_5+3_corrected VAEGDYTCYAQNTLGKDEMKVHLTVITAAPRIQSNKTNKRIKAGDTAVLDCSEVTGEPK
* *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

rat      PNVPWLLPSNNVISFSNDRFTFHANRTLSIHKVKPLDSGDYVCVAQNPSGDDTKTKYLDI
human_5+3_corrected PKIFWLLPNDMISFSIDRYTFHANGSLTINKVKPLDSGEYVCVARNPSGDDTKMYKLDV
* *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

rat      VSKPPLINGLYANKTVIKATAIRHKKYFDCRADGTPSSQVTNIMPNIPLPAPYFGSRV
human_5+3_corrected VSKPPLINGLYTNRTVIKATAVRHKKHFDCAEGTSPSEVMWIMPNDIPLTAPYFGSRI
*****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

rat      TVHPNGTLEMRNIRLSDSADFTCVVRSEGGESVLVVQLEVLEMLRRPTFRNPFNEKVIAQ
human_5+3_corrected TVHKNGTLEIRNVRLSDSADFTICVARNEGGEVLVVQLEVLEMLRRPTFRNPFNEKIVAQ
*** *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

rat      AGKPVALNCSVDGNPPPEITWILPDGTQFANRPNSFYLMAGNGSILLYKATRNKSGKYR
human_5+3_corrected LGKSTALNCSVDGNPPPEIWIWLENGTRFSNGEQSYQLIASNGSEFIISKTTREDAGKYR
* .. *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

rat      CAARNKVGYIEKLILLEIGQKPVILTYEPGMVKSVSSEPLSLHCVS DGI PKPNVKWTFPG
human_5+3_corrected CAARNKVGYIEKLIVILEIGQKPVILTYAPGT VKGISGESLSLHCVS DGI PKPNIKWTFPS
*****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

rat      GHVIDRPQVDGKYILHENGTLVLIKATTAHDQGNVICRAQNSVGQAVISVSVHVAYPPRI
human_5+3_corrected GYVVDLPQINGKYILLHDNGTLVKEATAYDRGNVICRAQNSVGHTLITVPEVMIVAYPPRI
* *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

rat      INYLPRMRLRTGEAMQLHCVALGIPKPKVTWETPRHSLLSKATARKPHRSEMLEHPOGTL
human_5+3_corrected TNRPPRSIVTRTGAAPQLHCVALGVFKPEITWEMPDSLLSTASKERTHGSEQLHLQGTIL
* * .. * *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

rat      VIQNLQTSDSGVYKCAQNLLGTDYATYIQVL
human_5+3_corrected VIQNPQTSDSGIYKCTAKNPLGSDYATYIQVI
**** *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

```

(rat: SEQ ID NO:13)

(human_5+3_corrected: SEQ ID NO:14)

Figure 17

MQKRGREVSCLLISLTAICLVVTPGSRVCPRRCACYPTEVHCTFRDLTSIPDGPANVER
 VNLGYNSLTRLTENDFSGLSRLELLMLHSNGIHRVSDKTFSGLQSLQVLKMSYNKVQIIE
 KDTLYGLRSLTRLHLDHNNIEFINPEAFYGLTLLRLVHLEGNRLTKLHPDTFVSLSYLQIF
 KTSFIKXLYLYDNFTSLPKEMVSSMPNLESYLHGNPWTCDCHLKWLSEWMQGNP
 (SEQ ID NO: 15)

Figure 18

MKVKGRGITCLLVSFAVICLVATPGGKACPRRCACYPTEVHCTFRYLTSIPDSIPPNVE
 RINLGYNLSLVRLMETDFSGLTKELELLMLHSNGIHTIPDKTFSDLQALQVLKMSYNKVRK
 LQKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYL
 QIFKISFIKFLYLSDNFLTSLPQEMSYPDLDSLLYLHGNPWTCDCHLRWLSDWIQPDVI
 KCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAAFQCAKPTIDSSLKSKSLTILEDSSS
 AFISPQGFMAPFGSLTLNMTDQSGNEANMVCSIQKPSRTSPIAFTEENDYIVLNTSFSTFL
 VCNIDYGHIPVWQILALYSDSPLILERSHLLSETPQLYYKYKVAPKPEDIFTNIEADLR
 ADPSWLMQDQISLQLNRTATTFTSLQIQYSSDAQITLPRAEMLPVKHKWTMISRDNNTK
 LEHTVLVGGTVGLNCPGQGDPTPHVDWLLADGSKVRAPYVSEDGRILIDKSGKLELQM
 ADSFDTGVYHCISSNYDDADILTYRITVVEPLVEAYQENGIHHTVFIGETLDLPCHSTGIP
 DASISWVIPGNNVLYQSSRDKKVLNNGTLRILQVTPKDQGYRCVAANPSGVDFLIFQV
 SVKMKGQRPLEHDGETEGSGLDESNPIAHLKEPPGAQLRTSALMEAEVKGHTSSTSKRH
 NYRELTQRRGDSTHRRFRENRRHFPPSARRIDPQHWAALEKAKKNAMPDKRENTTV
 SPPPVTQLPNIPGEEDDSSGMLALHEEFMVPATKALNLPARTVTADSRTISDSPMTNIN
 YGTEFSPVNSQILPPEEPTDFKLSTAILTTAMSKNINPTMSSQIQGTTNQHSSTVFPLLLG
 ATEFQDSDQMGRGREHFQSRPITVRTMIKDVNVKMLSSTTNKLLLESVNSHQTSVREV
 SEPRHNHFYSHTTQILSTSTFPSPDHTAAHSQFPIPRNSTVNIPLFRRFGRQRKIGGRGRIIS
 PYRTPVLRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSCLPRELTTATAALSFPSPAAPI
 TFPKADIARVPSEESTTLVQNPLLLLENKPSVEKTTPTIKYFRTEISQVTPTGAVMTYAPT
 SIPMEKTHKVNASYPRVSSTNEAKRDSVITSSLSGAITKPPMTIIAITRFSRRKIPWQQNFV
 NNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFRRLSTSVMQIPSNLTLT
 AHHTTTKTHNPGSLPTKKELFPPLNPMLPSIISKDSSTKSIISTQTAIPATTPTFPASVITYE
 TQTERSRAQTIQREQEPQKKNRDTPNISPDQSSGFTTPTAMTPPALAFTHSPPENTTGISST
 ISFHSRTLNLTDVIEELAQASTQTLKSTIASSETTLSSKSHQSTTTRKASLDTPIPPFLSSAT
 LMPVPISPPFTQRAVTDTRGDSHFRLMTNTVVKLHESSRHNLMQMPSSQLEPLTSSTSNLL
 HSTPMPALTTVKSQNSKLTPSPWAEQFWHKPYSDIAEKGGKPEVSMLATTGLSEATTLV
 SDWDGQKNTKKSDFDKKPVQEATTSKLLPFDLSRYIFEKPRIVGGKAASFTIPANSDAF
 LPCEAVGNPLPTIHWTRVSGLDLSRGNQNSRVQVLPNGTSLIQRVEIQDRFQYLCSASNL
 FGTDHLHVTLVSVSYPRIERRTKEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSE
 SSQGSRQAVVTVDGTLVLHNLISYDRGFYKCVASNPGGQDSSLVKIQVIAAPPVILEQRR
 QVIVGTWGESLKLPCAKGTPQPSVYWVLSDGTEVKPLQFTNSKLFLFSNGTLYIRNLAS

SDRFTYECIATSSTGSERRVVMLTMEERVTSPIREAASQKRTEVNFQDKLLLNCSATGEP
 KPQIMRLPSKAVVDQGSWIHYPNGSLFIGVTEKDSGVYLCVARNKMGDDLILMHVSLR
 LKPAKIDHKQYFRKQVLHGKDFQVDCASGSPVPEISWSLPDGTMINNAMQADDSGHR
 TRRYRLFNNGTLYFNKVGVAEEGDYTCYAQNTLGKDEMKVHLTVITAAPRIRQSNKTN
 KRIKAGDTAAVLDCEVTGDPKPKIFWLLPSNDMISFSIDRYTFHANGSLTINKVKLLDSG
 EYVCVARNPSGDDTKMYKLDVVSKEPLINGLYTNRTVIKATAVRHSHKHFDCAEGTP
 SPEVMWIMPDNIFLTAPYYGSRITVHKNGTLEIRNVRLSADFICVARNEGGEVLVVQLE
 VLEMLRRPTFRNPRNPFNEKIVAQLGKSTALNCVSDGNPPPEIHWILPNGTRFSNGPQSY
 QYLIASNGSFIISKTTREDAGKYRCAARNKVGYYEKLVIIEIGQKPVILTYAPGTVKGISGE
 SLSLHCVSDGIPKPNIKWTMPSGYVDRPQINGKYILHDNGTLVIKEATAYDRGNYICKA
 QNSVGHTLITVPMIVA YPPRITNRPPRSIVTRTGAAFQLHCV ALGVPKPEITWEMPDHS
 LLSTASKERTHGSEQLHLQGTLVIQNPQTSDSGIYKCTAKNPLGSDYAATYIQVI (SEQ ID
 NO: 16)

Figure 19

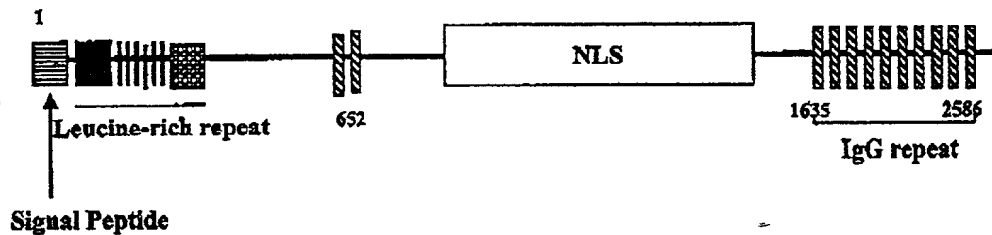


Figure 20

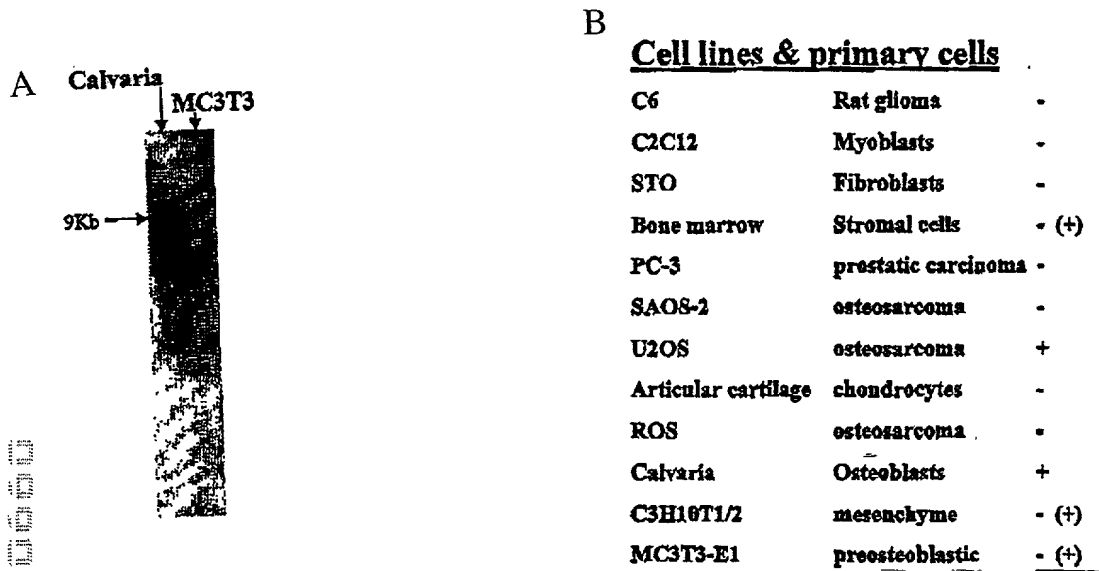
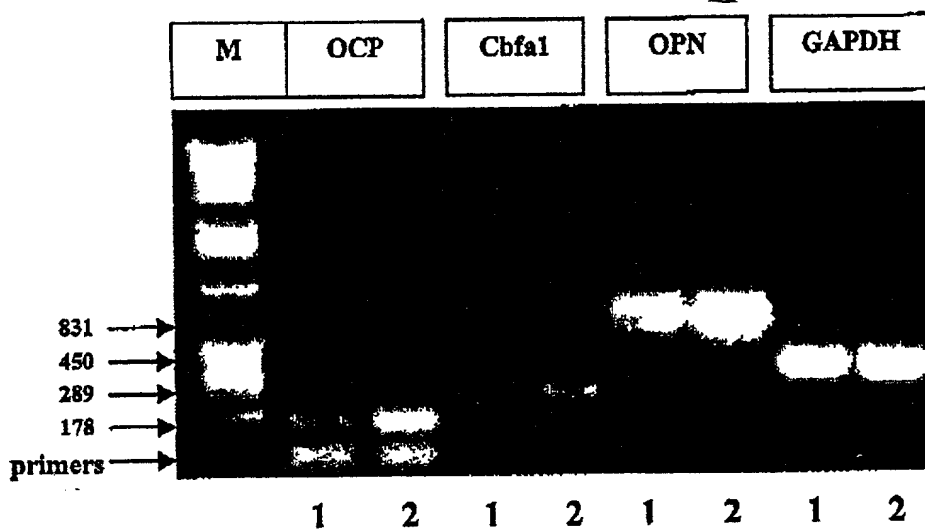


Figure 21



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Figure 24

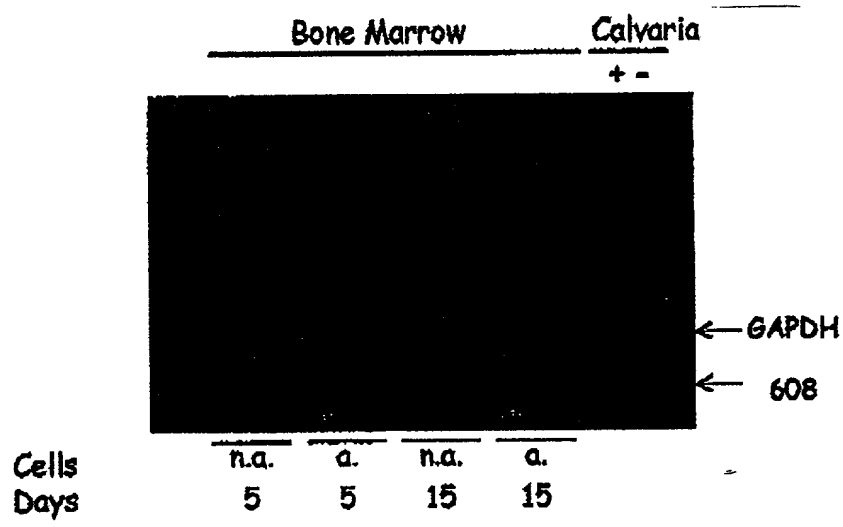
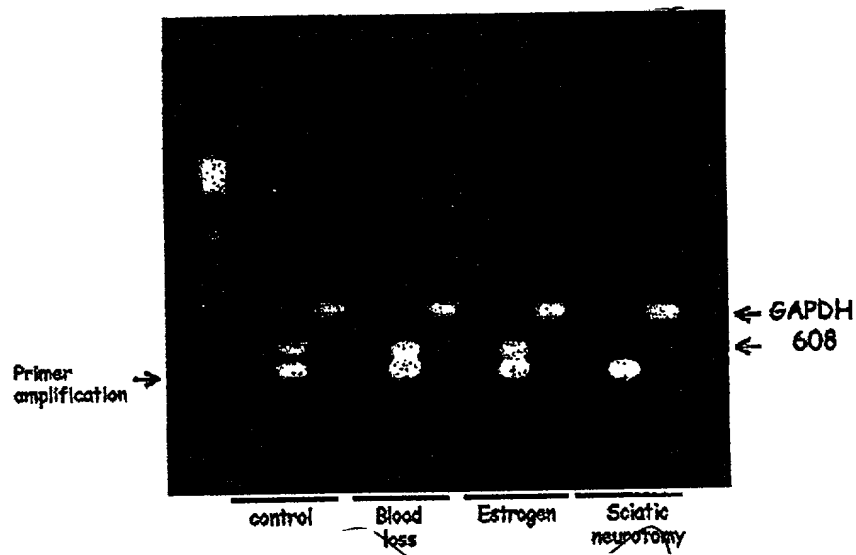


Figure 25



Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

A high-contrast, black and white photograph of a person standing, wearing a dark, textured garment. The image is heavily degraded with significant noise and artifacts, including a large white vertical streak down the center and a small circular mark near the bottom left.

Figure 27

A

B

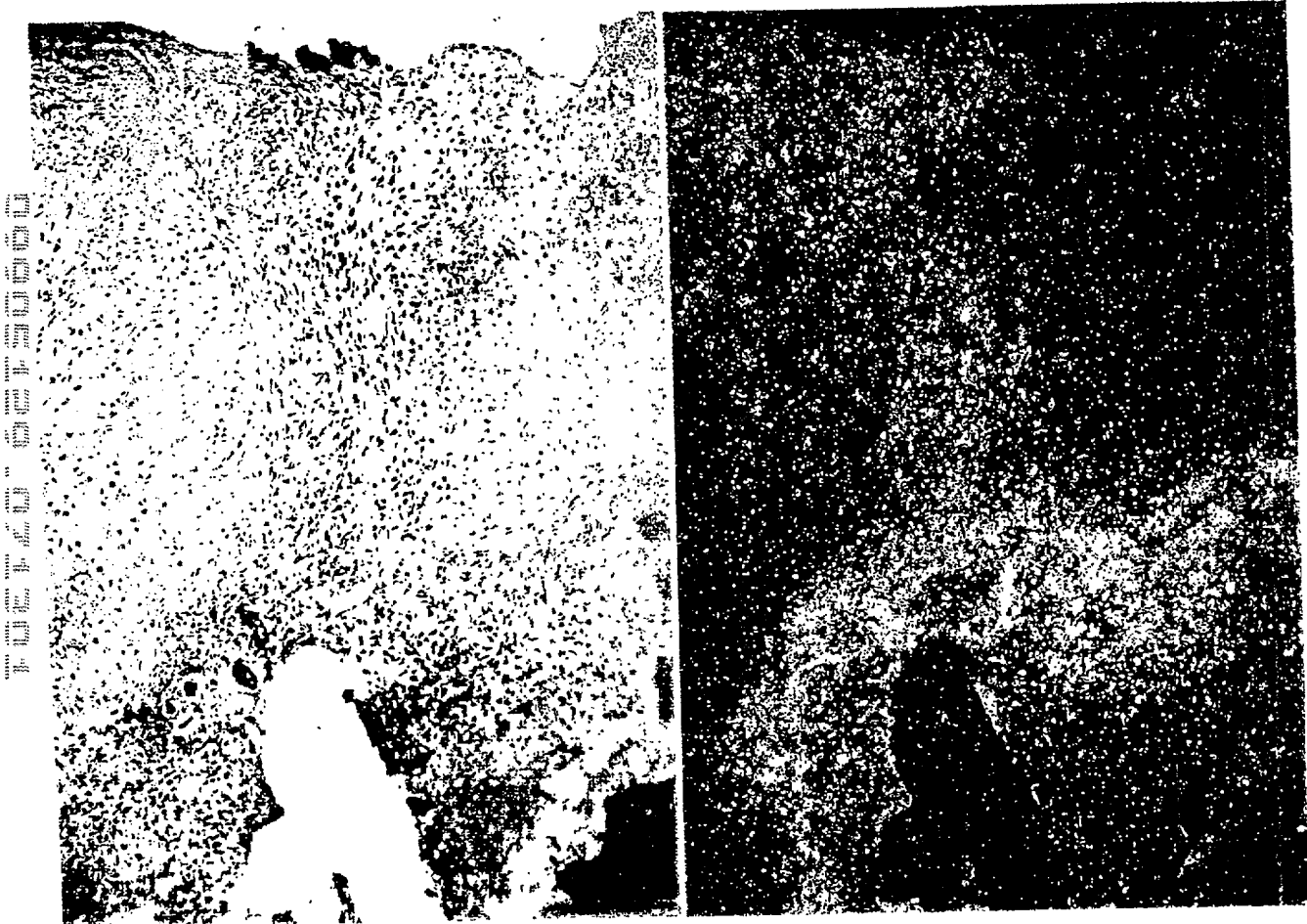
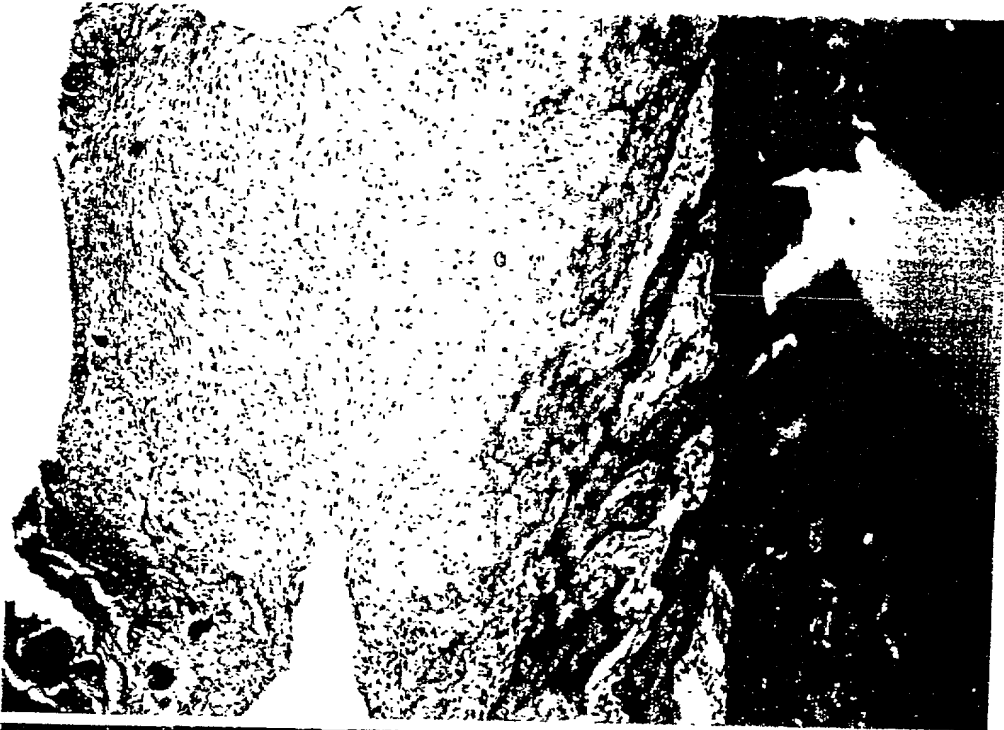


Figure 28

A

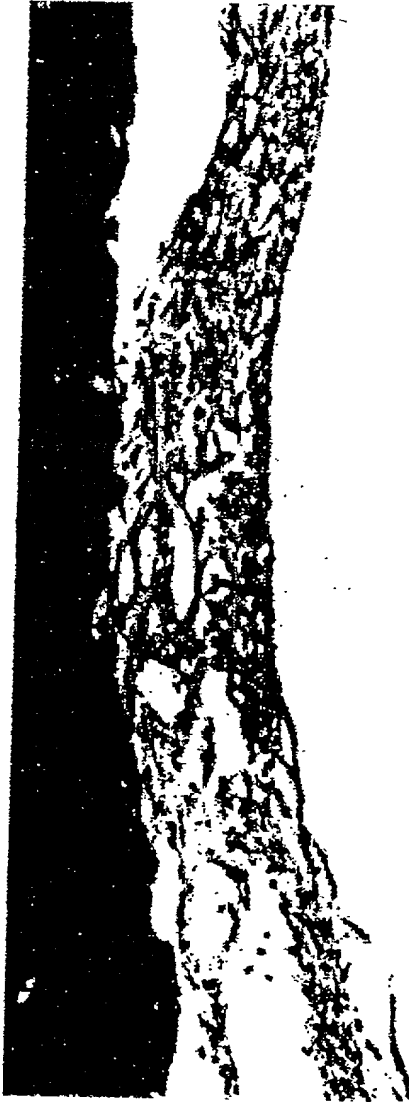


B



Figure 29

A



B



57/85

Figure 30

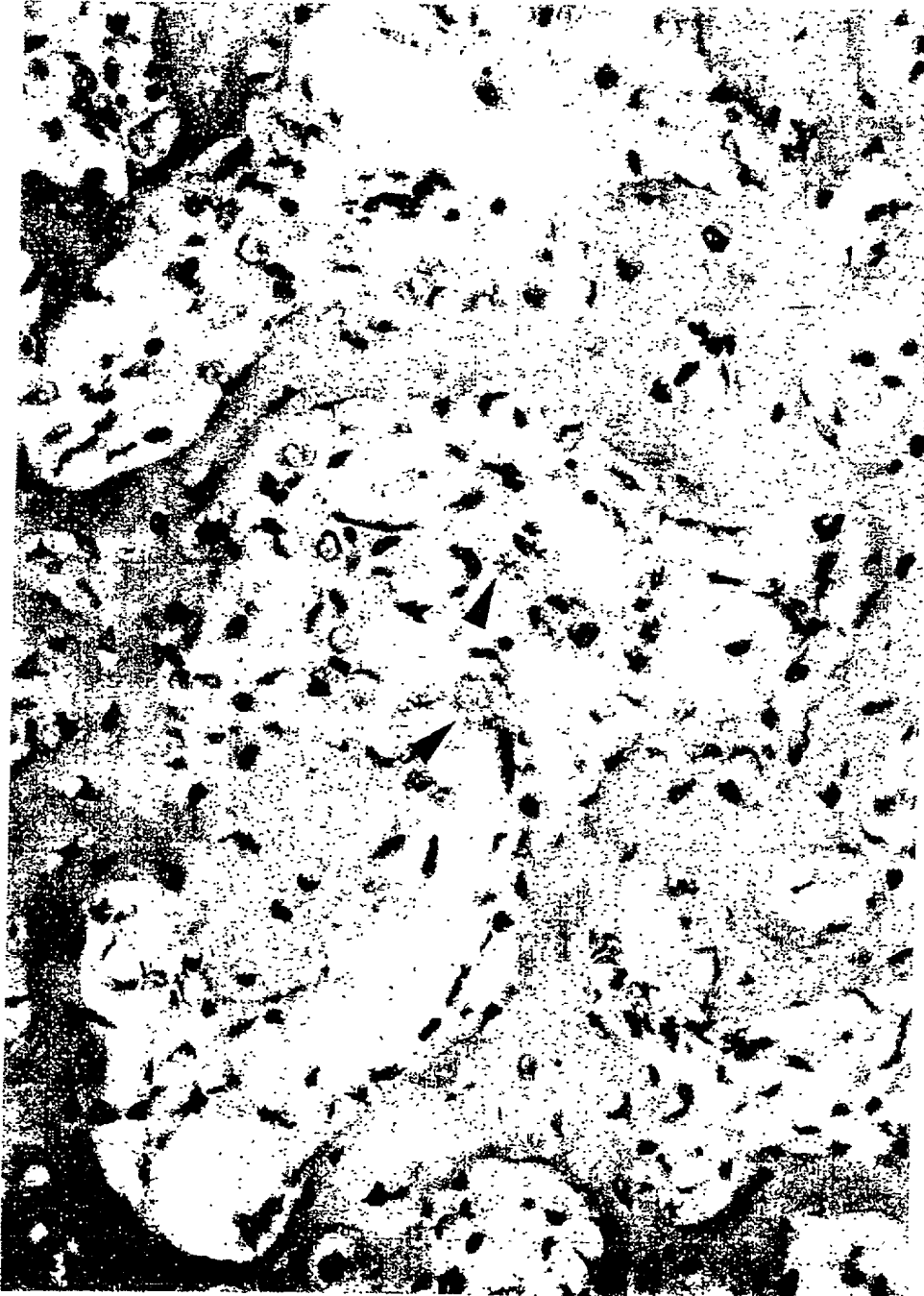
[illegible]

Figure 31

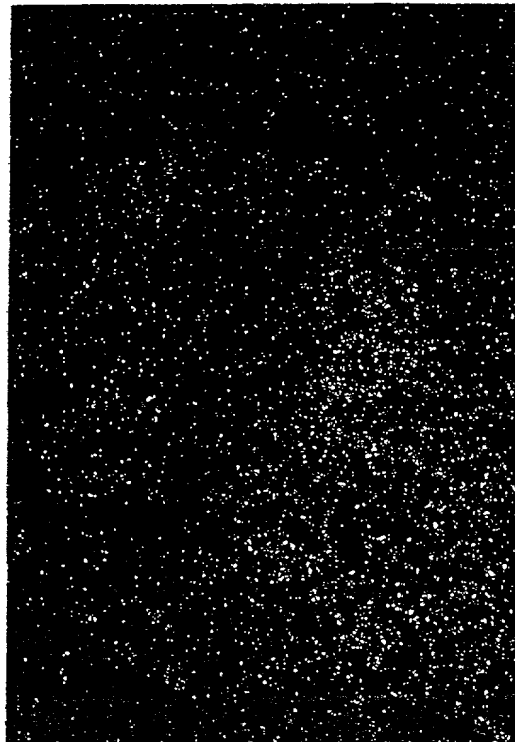


Figure 32

A



B



The image is a high-contrast, black-and-white scan of a textured surface. It appears to be a microscopic view or a heavily degraded document page. The background is a light, grainy white, and it is covered with a dense distribution of small, dark, irregular specks and fibers. These dark elements vary in size and shape, some appearing as thin, elongated fibers and others as small, rounded or angular particles. The overall effect is one of a granular or fibrous material. There are no discernible patterns, text, or other features that would allow for a more specific identification of the subject.

Figure 34

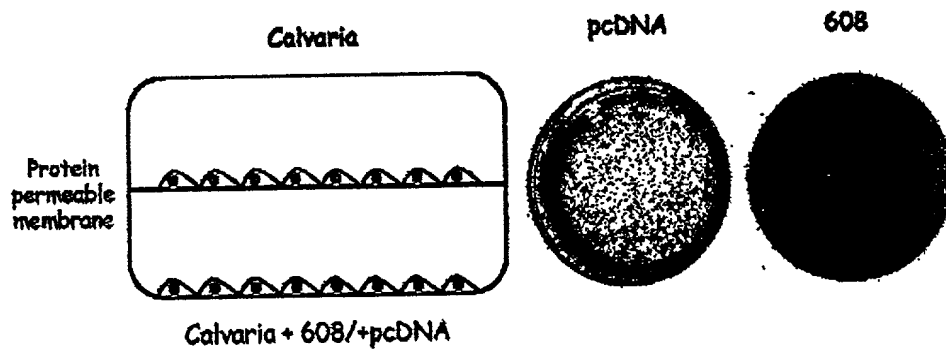


Figure 35

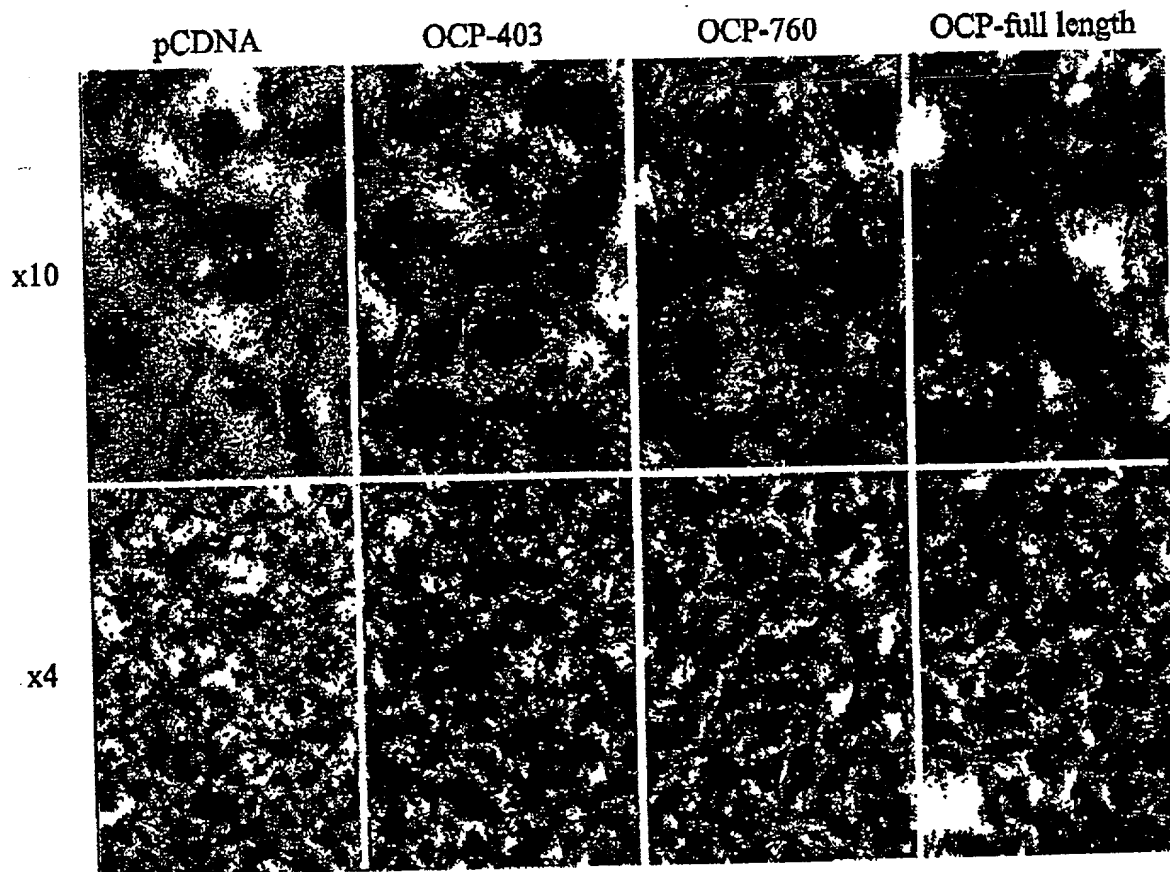


Figure 36

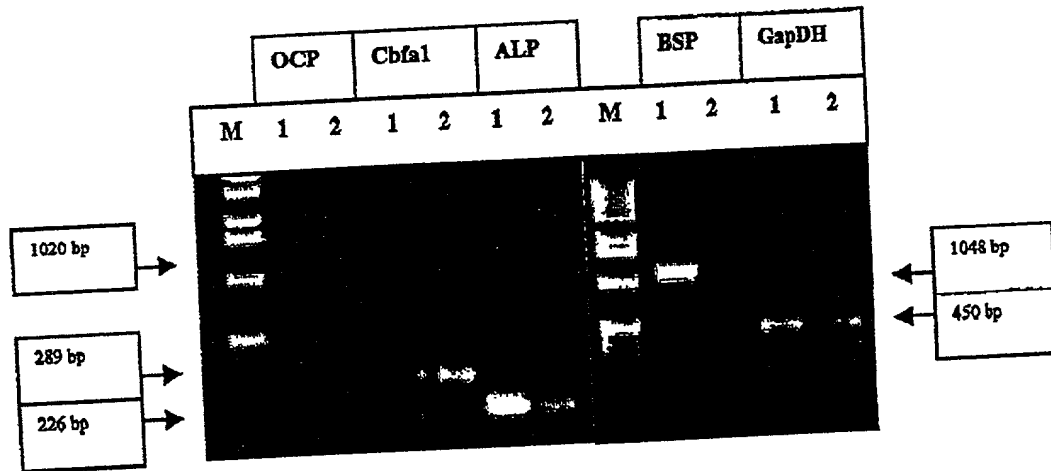


Figure 37

x 4

x 10

pCDNA
ROS stable line

OCP
ROS stable line



Figure 38

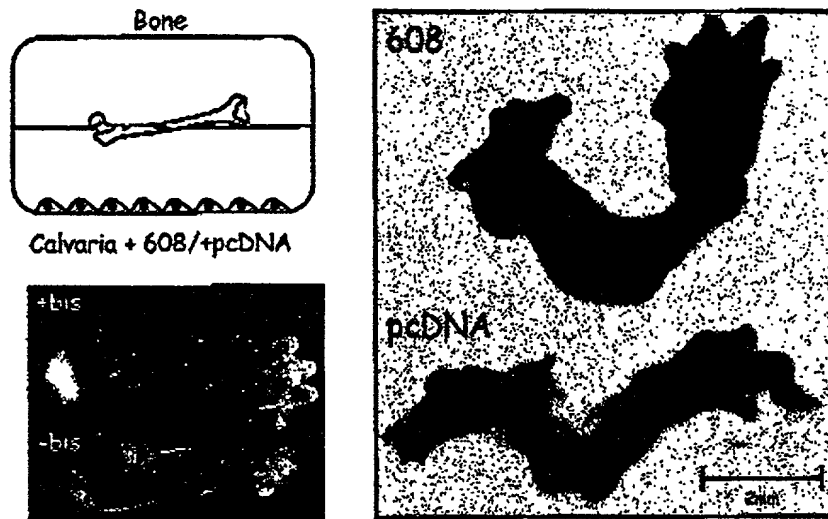


Figure 39

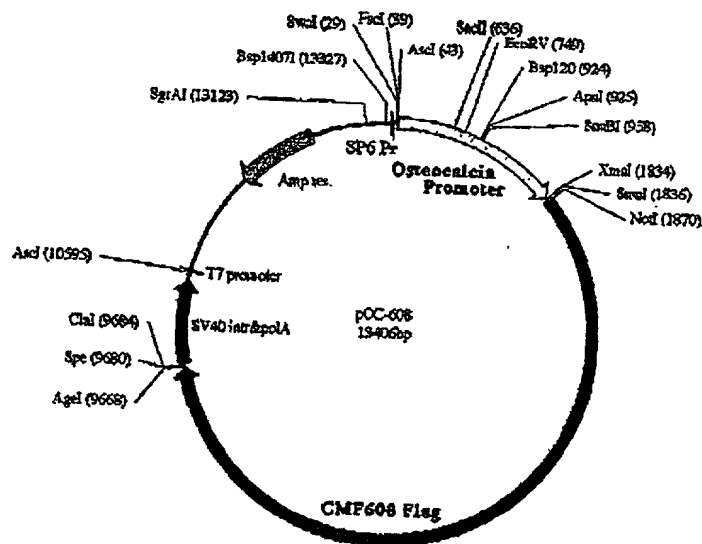


Figure 40

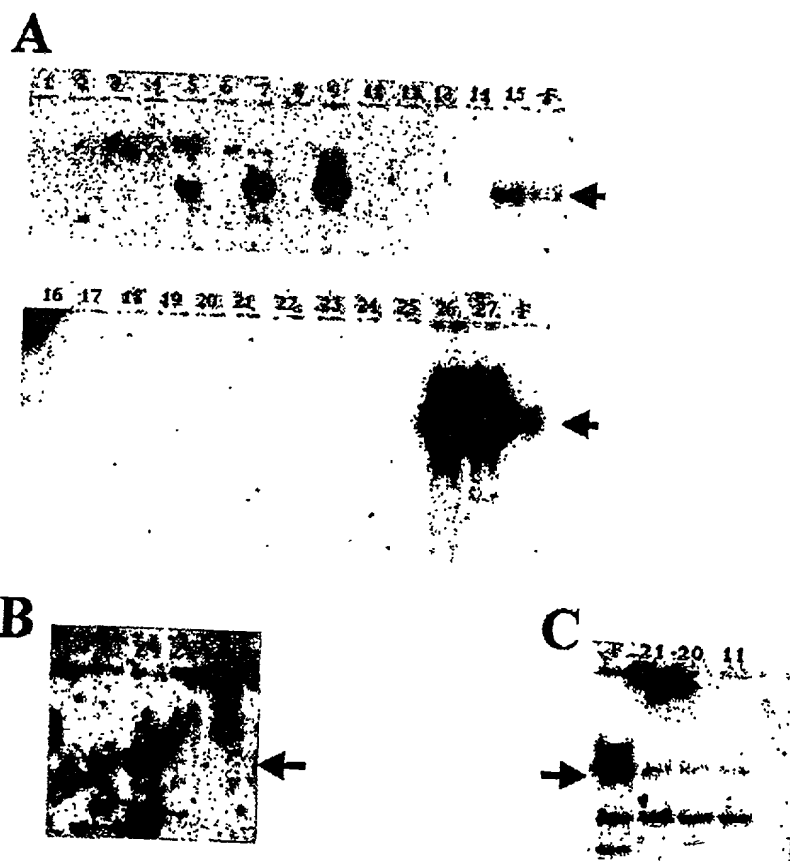


Figure 41

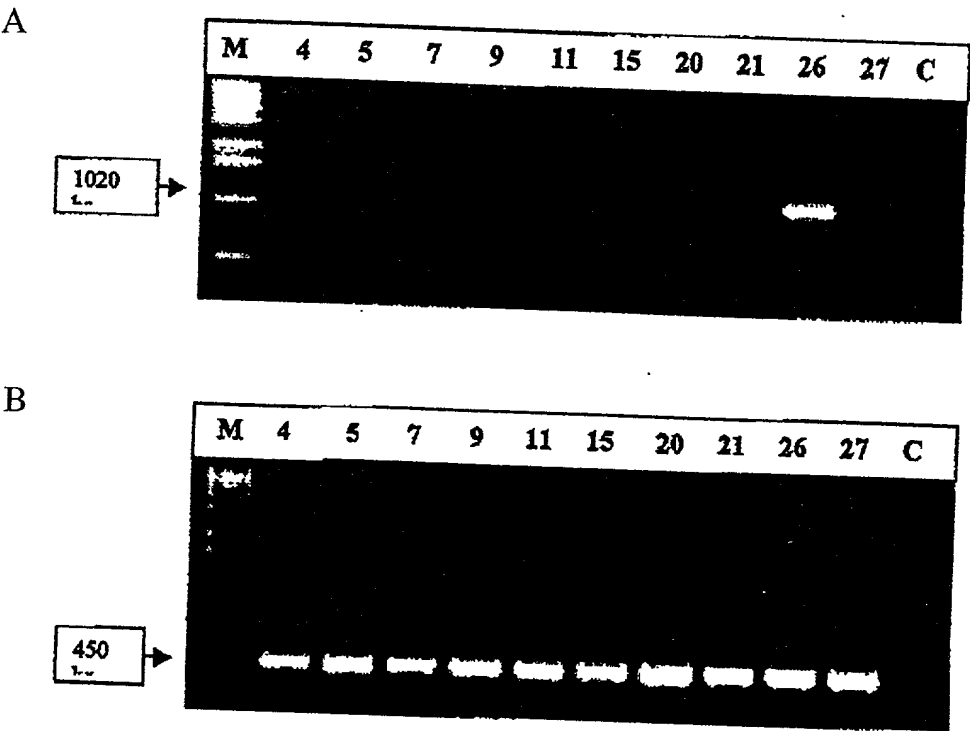
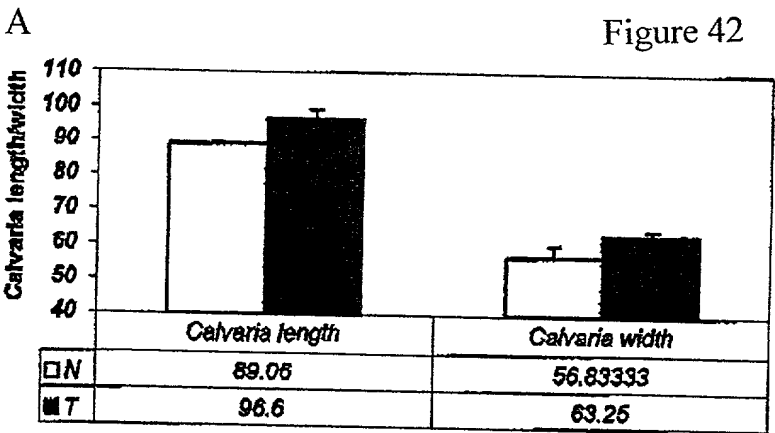


Figure 42



B

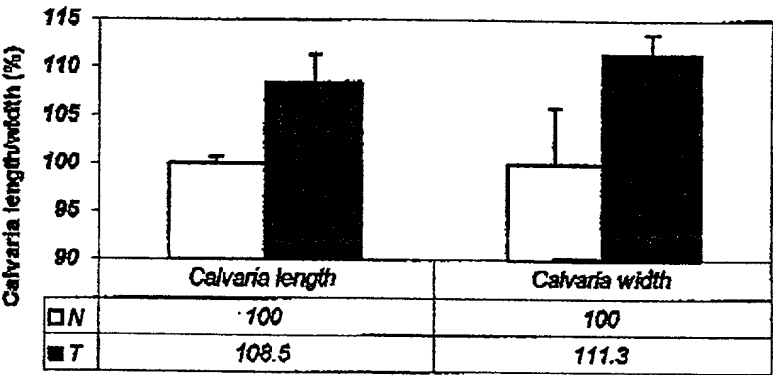


Figure 43

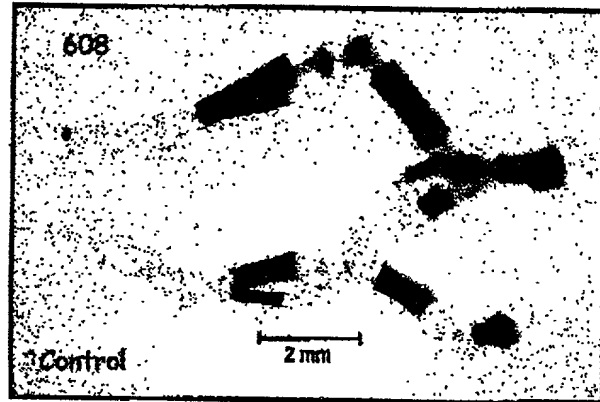


Figure 44

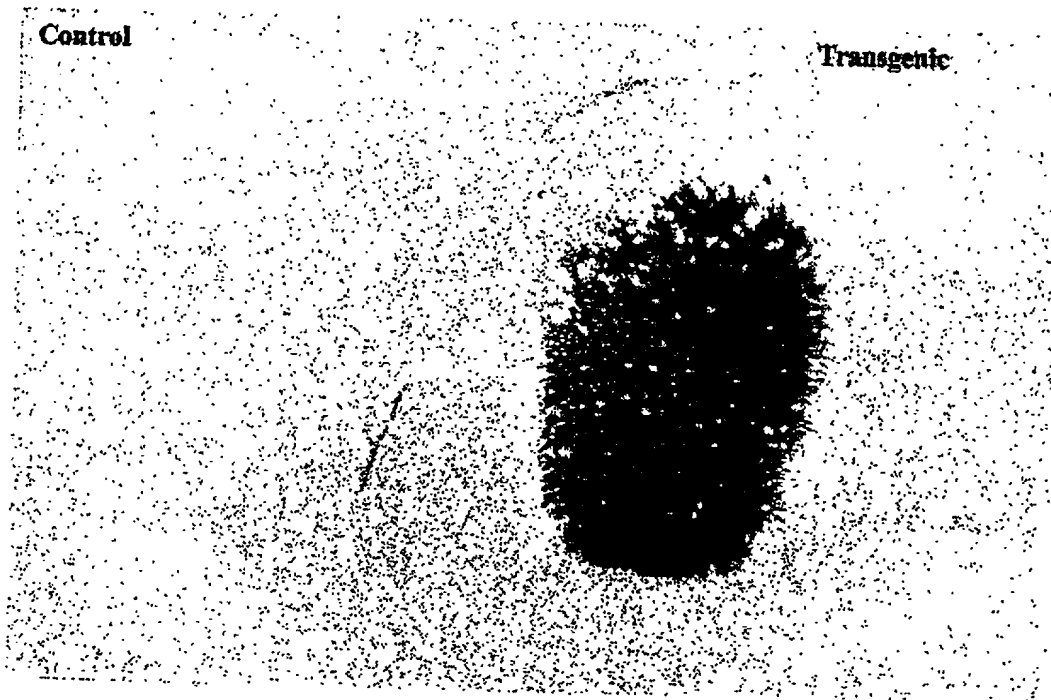
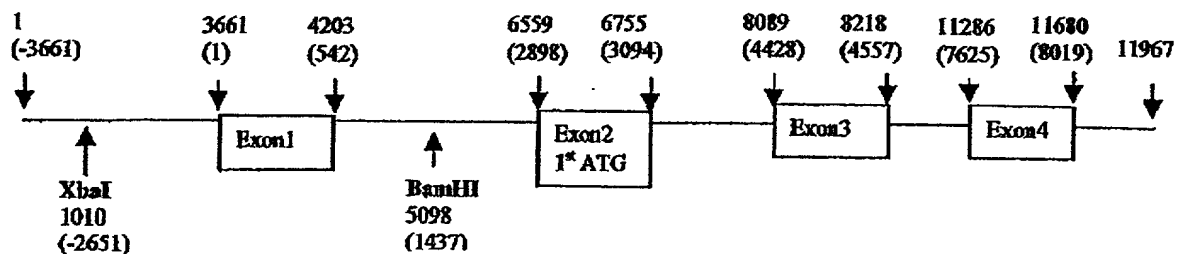


Figure 45



Clone 14C10 /15E11

T7 orientation in pKS

Figure 46

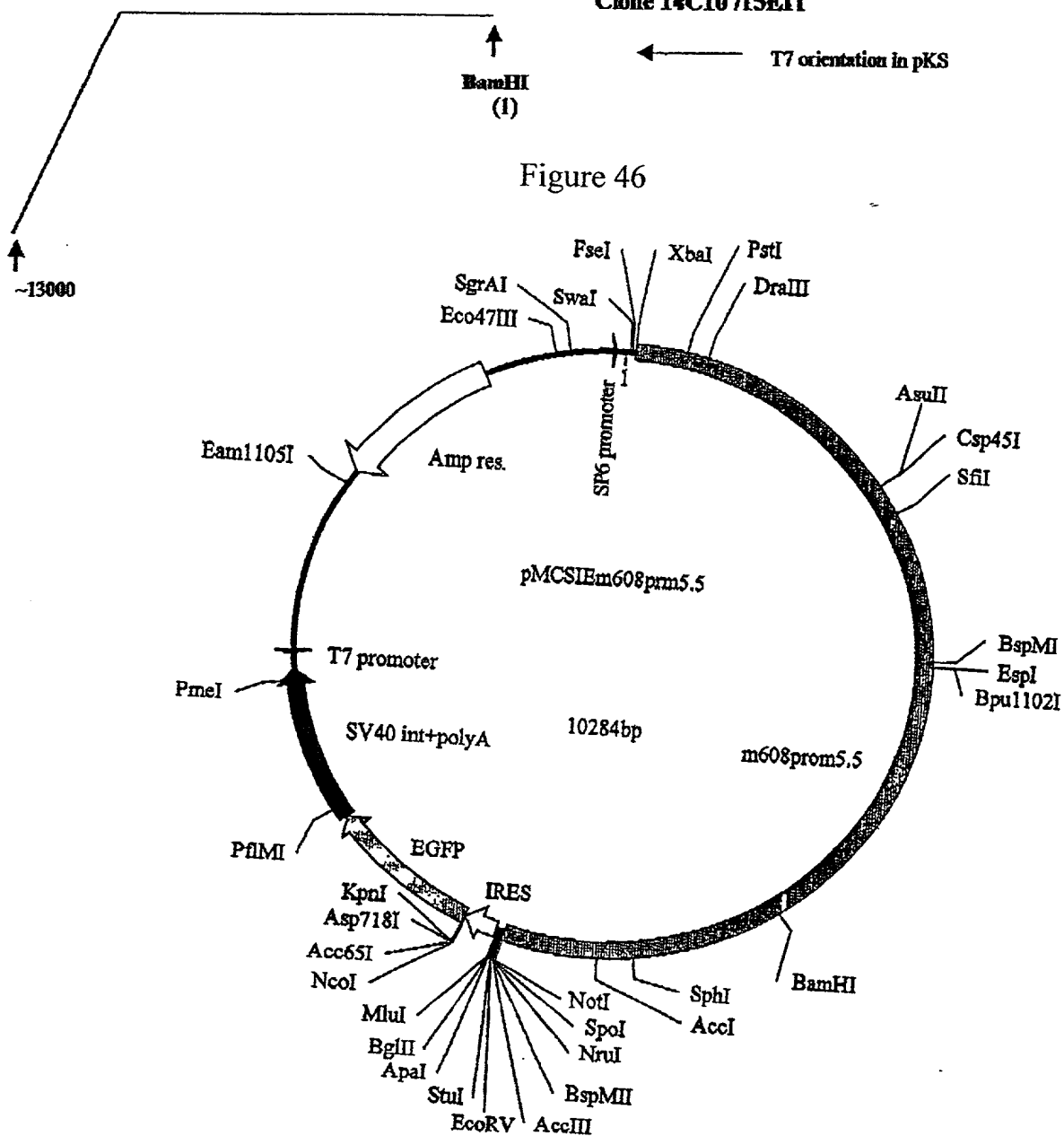


Figure 47

↓ (XbaI)

TCTAGAAGTAAATGATCCTGAGTAGCGATCCTGGGAAAATACGTA CTCTAACACACTGC
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 GTAGCTGCCCAGAACATACTAGATGCCATATTTCCAAGGCAAGTGTCCACATGCGGACAT
 CTTAAGAATATGGTTGTCTCTGCAGTGCTAAGGACCTTGTTCGTGCCACACAGGTCTCCAG
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 TTTCTAATCCATCAATTA AAAACCTTTAGAAATTTTGTAAACACAAAGATCCCTAGGCC
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 CCTCTCCCGAGTGAAGACCCCTAGAGGCTGAGCAGACCCCAAAGGCGGTGCAATTCCA
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Exon1

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 CACTGAGCCTTCGCCACGTGCGGGTTAAAGATATTTTCTAACAAGAGAAGCAGAATTCCTC
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 AGCAGACAGTGTATGCCTGCAAAAGTCAGAGACTCAGCCCTCCAGCTGGTCAGTTTACT
 GTCCTCCCGGTCATTAGTTGGCTCTGAAAAGGCCCATGTGTCCTTATTGGCAAGGACTTGC
 AGCAGTGTAGAAAGAAATTTGACCTTTTTTTCTAGTGGGTATTACAGCTGTAAAAGTAT
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 GATCATATAAAGAAGTACATTCATAAATGCAATGTGAAAAATATATATAATTTTATCTAT
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↓ (BamHI)

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 JAGTTACGACTCTTAAGAAAAATATCCCAATTATCCAGAGTTGCTATGTATGCTGTGC
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NotI site

(SEQ ID NO:17)

Figure 48

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(SEQ ID NO:18)

Figure 49

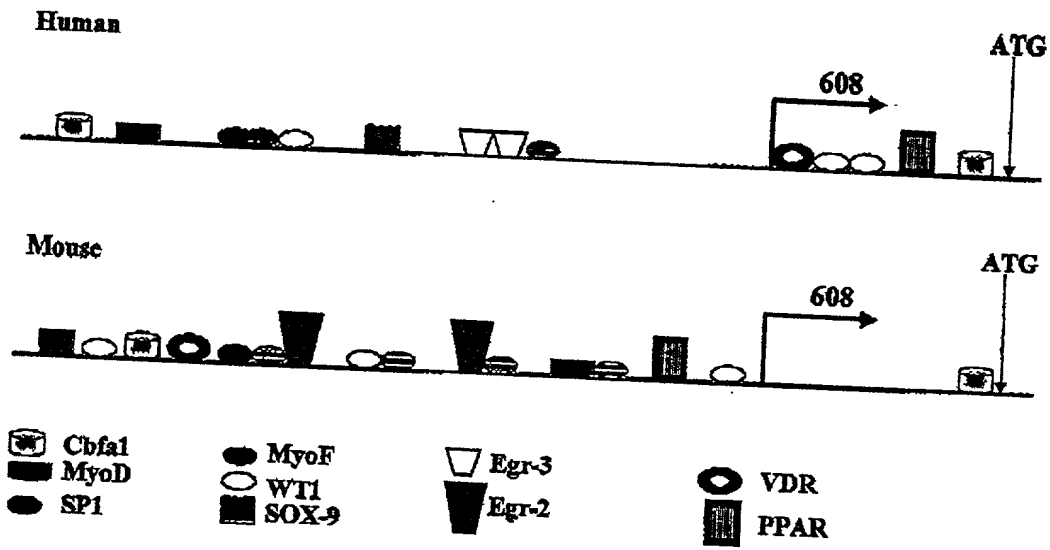


Figure 50

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AGCTCATCTGCTTTTTAATCATCACGCAGAGAGTATTCAAAAATATTCAGTGATGTA
ACAGTGACAGTGTAGGCATAGAAGTAATCATTAGTAAATCTTAATATGGGTAAACT
CATTCATAACAGCTCCAGGTTGG (SEQ ID NO:19)

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 CTCAACTCTTTAAGCAAACAATGCTGTTGTTTCATGAAAAGCACAATAAAGTACATAT
 GTCCCATAATATTCATCAAAATTTGCATGCAGCACATAATAGCAATCAAAGCAATAA
 CACCCACTGTTTCACAGAGACTTTAAACATGAAACTGGAACCTATGTCTAGTGTTTTGA
 CTTAGGGTACATAGTATGCTGTGTCTGTATGTACCAATGTTGATTTAGGTCATCAGA
 CAGCATTTGGAACATGTATCTTCAGGAGGAATCATTTCATGTATCCTGCATGAAATTC
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 AGGTTTTACTCCCAGGTAACATTTAGGGAAAAGCTGTCTATGTTCTCAGTTTGGCTTT
 TATTTATGAGGGATGTTGGTATTCCAGAAAATTCTCTTTTGAAGAGATTACAATTTA
 GGTCAAAACAGAAAAATATGTAAAAAGTTATTGTTTTTATTAGTATTTTCATGTTCTTT
 TCTTTTTTAAAAATGGTATGCTTAGAACTAATTAAGATTAGATTAGATTAGATTAGA
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 TTAATAAAAAAAAAAACTATTGATGTGGAATGATCTTAATTTGGGGAAAAGACAATT
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 ACCAGCATGCTGTGCTCTGAGAAGGGCCTAATGAAGGGGCAGGAGGAAGTGAAATG
 AGATGGTAGAAAGGAAGTCATATACCATGGCTTCTCTCGTGGGTGGAATCTAGAT
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 GGAGTGAGGGAGACAATAGGAACCAATGAGAGGCAAAGTTCATGGTCAATGTGTGT
 GGAGACACCATAATAAACTCCTTTTTTGTGTTGCTAACTAAAACCACTAAAATCTAA
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CATCACTAATGCTTTTCACCATACACAAATGTAGGCAGAAGAGTGTAATCCACTTAG
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GACAGTGAGAGGGAAATGAACAAGAAAAAATGTGGACACATGCACAAAAATTCCA
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GTCACATTTAGTTGGCAACTACTTTGTTTGAATTGAGTTGGAGTTAAGGTCCCATAG
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CCTGGATCACAAACATTGAGTTTATCAACCCCGAGGCGTTTTACGGACTCACCTT
GCTCCGCTTGGTACATCTAGAAGGAAACCGGCTGACAAAGCTCCATCCAGACACAT
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GTATGATAACTTCATTGACCTCCCTCCCAAAGAAATGGTCTCCTCTATGCCAAACC
TAGAAAGCCTTTACTTGCATGGAAACCCATGGACCTGTGACTGCCATTTAAAGTGGT
TGTCCGAGTGGATGCAGGGAAACCCAGGTAACCTATCTTGTGTTTGTGTTTCTTTTTTT
ATARKACGTATTTTCCTCAATTTCAATTTAGAATGATATCCCAAAGTCCCCCATAACC
TCCCCCCCCACTTCCCTACCTACCATTTCCCATTTTTTTGGCCCTGGCATTCCCCTGTACT
GGGGCATATAAAGTTTGCCTGTCCAATGGACCTCTCTTTCCAGTGATGGCCAACTAG
GCCATCTTTTGATACATATGCAGCTAGAGTCAAGAGCTCTGGGGTACTGGTTAGTTC
ATAATGTTGTTGCACCTACAGGGTTGAA (SEQ ID NO:20)

Figure 51

MPKRAHWGALS VV LILL WGHPRVALACPHPCACYVPSEVHCTFRSLASVPAGIARHVE
 RINLGFNSIQALSETSFAGLTKLELLMIHGNEIPSIPDGALRDLSSLQVFKFSYNKLRVITG
 QTLQGLSNLMRLHIDHNKIEFIHPQAFNGLTSLRLLHLEGNLLHQLHPSTFSTFTFLDYFR
 LSTIRHLYLAENMVRTLPA SMLRNMPLLENLYLQGNPWTCDCEMRWFLEWDAKSRGIL
 KCKKDKAYEGGQLCAMCFSPKKLYKHEIHKLKDMTCLKPSIESPLRQNRSR SIEEEQEQ
 EEDGGSQ LILEKFQLPQWSISLNM TDEHGNMVNL VCDIKKPM DVYKIHNLNQTDP DIDIN
 ATVALDFECPMTRENYEKLWKLIA YYSEVPVKLHRELMLS KDPRVSYQYRQDADEEAL
 YYTG VRAQILAEP EWVMQPSIDIQLNRRQSTAKKVLLSYYTQYSQTISTK DTRQARGRS
 WVMIEPSGAVQRDQTVLEGGPCQLSCNVKASESPSIFWVLPDGSILKAPMDDPD SKFSIL
 SSGWLRIKSMEPSDSGLYQCIAQVRDEMDRMVYRVLVQSPSTQPAEKDVTVTIGKNPGES
 VTLPCNALAIP EAHLSWILPNRRINDLANTSHVYMLPNGTLSIPKVQVSDSGYYRCVAV
 NQQGADHFTV GITVTKKGSGLPSKRGRRPGAKALSRVREDIVEDEGGSGMGDEENTSR
 RLLHPKDQEVFLKTKDDAINGDKKAKKGRRKLKLWKHSEKEPETNVAEGRRVFESRRR
 INMANKQINPERWADILAKVRGKNLPKGTEVPPLIKTTSPPSLSLEVTPPFPAVSPPSASP
 VQTVTSAEESSADVPLL GEEHVLTGISSASMGLEHNHNGVILVEPEVTSTPLEEVVDDL
 SEKTEEITSTEGDLKGTAAPT LISEPYEPSPTLHTLDTVYEKP THEETATEGWSAADVGSS
 PEPTSSEYEPPLDAVSLAESEPMQYFDPDLET KSQPDDEKMKEDTFAHLTPTPTIWNDS
 STSQLFEDSTIGEPGVPGQSHLQGLTDNIHLVKSSLSTQDTLLIKKG MKEMSQTLQGGNM
 LEGDPTHSRSSSESEGQESKSITLPDSTLGIMSSMSPVKKPAETT VGTLLDKDTT VTTTPR
 QKVAPSSTMSTHPSRRRPNGRRRLRPNKFRHRHKQTPPTTFAPSETFSTQPTQAPDIKISS
 QVSSLVPTAWVDNTVNTPKQLEMEKNAEPTSKGT PRRKHGKRPNKHRYTPSTVSSRA
 SGSKPSPSPENKHRNIVTPSSETILLPRTVSLKTEGPYDSLDMYTTTRKIYSSYPKVQETLP
 VTYKPTSDGKEIKDDVATNVDKHKSDILVTGESITNAIPTSRSLVSTMGEFKEESSPVGFP
 GTPTWNPSRTAQPGRLQTDIPVTTSGENLTD PPLLKELEDVDFTSEFLSSLTVSTPFHQEE
 AGSSTTLSSIKVEVASSQAETTTLDQDHLETTVA ILLSETRPQNHTPTAARMKEPASSPS
 TILMSLGQTTTTK PALPSPRISQASRDSKENVFLNYVGNPETEATPVNNEGTOHMSGPNE
 LSTPSSDRDAFNLSTKLELEKQVFGSRSLPRGPDSQRQDGRVHASHQLTRVPAKPILPTA
 TVRLPEMSTQSASRYFVTSQSPRHWTNKPEITTYPSGALPENKQFTTPRLSSTTIPLPLHM
 SKPSIPSKFTDRRTDQFNGYSKVFGNNNIPEARNPVGKPPSPRIPHYSNGRLPFFTNKTL SF
 PQLGVTRRPQIPTSPAPVMRERKVIPGSYNRIHSHSTFHLDFGPPAPPLLHTPQTTGSPSTN
 LQNIPMVSSTQSSISFITSSVQSSGSFHQSSSKFFAGGPPASKFWSLGEKPQILTKSPQTVSV
 TAETDTVFPCEATGKPKPFVTWTKVSTGALMTPNTRIQRFEVLKNGTLVIRKVQVQDRG
 QYMCTASNLHGLDRMVVLLSVTVQQPQILASHYQDVTVYLGDTIAMECLAKGTPAPQI
 SWIFPDRRVWQTVSPVESRITLHENRTLSIKEASFS DRGVYKCVASNAAGADSLAIRLHV
 AALPPVIHQEKLENISLPPGLSIHIHCTAKAAPLPSVRWVLGDGTQIRPSQFLHGNLFVFP
 NGTLYIRNLAPKDSGRYECVAANLVGSARRTVQLNVQRAAANARITGTSPRRTDVRYG
 GTLKLDCSASGDPWPRILWRLPSKRMIDALFSFDSRIKVFANGTLVVKSVTDK

DAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEENDHKVIFYGGDLKVDCVATGL
PNPEISWSLPDGSLVNSFMQSDDSGGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAEN
QVGKDEMRRVRVKVVTAPATIRNKTYLAVQVPYGDVVTVACEAKGEPMPKVTWLSPTN
KVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGEDRKTVWIHVNVQPPKING
NPNPITTVREIAAGGSRKLIDCKAEGIPTPRVLWAFPEGVVLPAPIYYGNRITVHGNGSLDI
RSLRKSDSVQLVCMARNEGGEARLIVQLTVLEPMKPIFHDPISEKITAMAGHTISLNCS
AAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLHISGLSSVDAGAYRCVARNAA
GHTERLVSLKVGLKPEANKQYHNLVSIINGETLKLPPGAGQGRFSWTLPNGMHLEG
PQTLGRVSLLDNGTLTVREASVFDRTYVCRMETEYGPSVTSIPVIVIAYPTRITSEPTPI
YTRPGNTVKLNCMAMGIPKADITWELPKSHLKAGVQARLYGNRFLHPQGSLLTIQHAT
QRDAGFYKCMANKILGSDSKTTYIHVF (SEQ ID NO: 21)

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Figure 52

ATGCCCAAAG CCGCGCACTG GGGGGCCCTC TCCGTGGTGTC TGATCCTGCT
TTGGGGCCAT CCGCGAGTGG CGCTGGCCTG CCCGCATCCT TGTGCCTGCT
ACGTCCCCAG CGAGGTCCAC TGCACGTTCC GATCCCTGGC TTCCGTGCCC
GCTGGCATTG CTAGACACGT GGAAAGAATC AATTTGGGGT TTAATAGCAT
ACAGGCCCTG TCAGAAACCT CATTTGCAGG ACTGACCAAG TTGGAGCTAC
TTATGATTCA CGGCAATGAG ATCCCAAGCA TCCCCGATGG AGCTTTAAGA
GACCTCAGCT CTCTTCAGGT TTTCAAGTTC AGCTACAACA AGCTGAGAGT
GATCACAGGA CAGACCCTCC AGGGTCTCTC TAACTTAATG AGGCTGCACA
TTGACCACAA CAAGATCGAG TTTATCCACC CTCAAGCTTT CAACGGCTTA
ACGTCTCTGA GGCTACTCCA TTTGGAAGGA AATCTCCTCC ACCAGCTGCA
CCCCAGCACC TTCTCCACGT TCACATTTTT GGATTATTT AGACTCTCCA
CCATAAGGCA CCTCTACTTA GCAGAGAACA TGGTTAGAAC TCTTCCTGCC
AGCATGCTTC GGAACATGCC GCTTCTGGAG AATCTTTACT TGCAGGGAAA
TCCGTGGACC TCGGATTGTG AGATGAGATG GTTTTTGGAA TGGGATGCAA
AATCCAGAGG AATTCTGAAG TGTA AAAAGG ACAAGCTTA TGAAGGCGGT
CAGTTGTGTG CAATGTGCTT CAGTCCAAAG AAGTTGTACA AACATGAGAT
ACACAAGCTG AAGGACATGA CTTGTCTGAA GCCTTCAATA GAGTCCCCTC
TGAGACAGAA CAGGAGCAGG AGTATTGAGG AGGAGCAAGA ACAGGAAGAG
GATGGTGGCA GCCAGCTCAT CCTGGAGAAA TTCCA ACTGC CCCAGTGGAG
CATCTCTTTG AATATGACCG ACGAGCACGG GAACATGGTG AACTTGGTCT
GTGACATCAA GAAACCAATG GATGTGTACA AGATTCACTT GAACCAAACG
GATCCTCCAG ATATTGACAT AAATGCAACA GTTGCCTTGG ACTTTGAGTG
TCCAATGACC CGAGAAA ACT ATGAAAAGCT ATGGAAATTG ATAGCATACT
ACAGTGAAGT TCCCGTGAAG CTACACAGAG AGCTCATGCT CAGCAAAGAC
CCCAGAGTCA GCTACCAGTA CAGGCAGGAT GCTGATGAGG AAGCTCTTTA
CTACACAGGT GTGAGAGCCC AGATTCTTGC AGAACCAGAA TGGGTCATGC
AGCCATCCAT AGATATCCAG CTGAACCGAC GTCAGAGTAC GGCCAAGAAG
GTGCTACTTT C TACTACAC CCAGTATTCT CAAACAATAT CCACCAAAGA
TACAAGGCAG GCTCGGGGCA GAAGCTGGGT AATGATTGAG CCTAGTGGAG
CTGTGCAAAG AGATCAGACT GTCCTGGAAG GGGGTCCATG CCAGTTGAGC
TGCAACGTGA AAGCTTCTGA GAGTCCATCT ATCTTCTGGG TGCTTCCAGA
TGGCTCCATC CTGAAAGCGC CCATGGATGA CCCAGACAGC AAGTTCTCCA
TTCTCAGCAG TGGCTGGCTG AGGATCAAGT CCATGGAGCC ATCTGACTCA
GGCTTGTACC AGTGCATTGC TCAAGTGAGG GATGAAATGG ACCGCATGGT
ATATAGGGTA CTTGTGCAGT CTCCCTCCAC TCAGCCAGCC GAGAAAGACA
CAGTGACAAT TGGCAAGAAC CCAGGGGAGT CGGTGACATT GCCTTGCAAT
GCTTTAGCAA TACCCGAAGC CCACCTTAGC TGGATTCTTC CAAACAGAAG
GATAATTAAT GATTTGGCTA ACACATCACA TGTATACATG TTGCCAAATG
GAACTCTTTC CATCCCAAAG GTCCAAGTCA GTGATAGTGG

TTACTACAGA TGTGTGGCTG TCAACGACGA AGGGGCAGAC CATTTCACGG
TGGAATCAC AGTGACCAAG AAAGGGTCTG GCTTGCCATC CAAAAGAGGC
AGACGCCAG GTGCAAAGGC TCTTCCAGA GTCAGAGAAG ACATCGTGGA
GGATGAAGGG GGCTCGGGCA TGGGAGATGA AGAGAACACT TCAAGGAGAC
TTCTGCATCC AAAGGACCAA GAGGTGTTCC TCAAAACAAA GGATGATGCC
ATCAATGGAG ACAAGAAAGC CAAGAAAGGG AGAAGAAAGC TGAAACTCTG
GAAGCATTCG GAAAAAGAAC CAGAGACCAA TGTTGCAGAA GGTCGCAGAG
TGTTTGAATC TAGACGAAGG ATAAACATGG CAAACAAACA GATTAATCCG
GAGCGCTGGG CTGATATTTT AGCCAAAGTC CGTGGGAAAA ATCTCCCTAA
GGGCACAGAA GTACCCCGT TGATTA AAC CACAAGTCCT CCATCCTTGA
GCCTAGAAGT CACACCACCT TTCTCTGCTG TTTCTCCCC CTCAGCATCT
CCTGTGCAGA CAGTAACCAG TGCTGAAGAA TCCTCAGCAG ATGTACCTCT
ACTTGGTGAA GAAGAGCACG TTTTGGGTAC CATTTCTCA GCCAGCATGG
GGCTAGAACA CAACCACAAT GGAGTTATTC TTGTTGAACC TGAAGTAACA
AGCACACCTC TGGAGGAAGT TGTTGATGAC CTTTCTGAGA AGACTGAGGA
GATAACTTCC ACTGAAGGAG ACCTGAAGGG GACAGCAGCC CCTACACTTA
TATCTGAGCC TTATGAACCA TCTCTACTC TGCACACATT AGACACAGTC
TATGAAAAGC CCACCCATGA AGAGACGGCA ACAGAGGGTT GGTCTGCAGC
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TGGATGCTGT CTCCTTGGCT GAGTCTGAGC CCATGCAATA CTTTGACCCA
GATTTGGAGA CTAAGTCACA ACCAGATGAG GATAAGATGA AAGAAGACAC
CTTTGCACAC CTTACTCCAA CCCCCACCAT CTGGGTAAAT GACTCCAGTA
CATCACAGTT ATTTGAGGAT TCTACTATAG GGGAACCAGG TGTCCCAGGC
CAATCACATC TACAAGGACT GACAGACAAC ATCCACCTTG TGAAAAGTAG
TCTAAGCACT CAAGACACCT TACTGATTAA AAAGGGTATG AAAGAGATGT
CTCAGACACT ACAGGGAGGA AATATGCTAG AGGGAGACCC CACACACTCC
AGAAGTTCTG AGAGTGAGGG CCAAGAGAGC AAATCCATCA CTTTGCCTGA
CTCCACACTG GGTATAATGA GCAGTATGTC TCCAGTTAAG AAGCCTGCGG
AAACCACAGT TGGTACCCTC CTAGACAAAG ACACCACAAC AGTAACAACA
ACACCAAGGC AAAAAGTTGC TCCGTCATCC ACCATGAGCA CTCACCCTTC
TCGAAGGAGA CCAAACGGGA GAAGGAGATT ACGCCCCAAC AAATTCCGCC
ACCGGCACAA GCAAACCCCA CCCACAACCTT TTGCCCCATC AGAGACTTTT
TCTACTCAAC CAACTCAAGC ACCTGACATT AAGATTTCAA GTCAAGTGGA
GAGTTCTCTG GTTCCTACAG CTTGGGTGGA TAACACAGTT AATACCCCA
AACAGTTGGA AATGGAGAAG AATGCAGAAC CCACATCCAA GGGAACACCA
CGGAGAAAAC ACGGGAAGAG GCCAAACAAA CATCGATATA CCCCTTCTAC
AGTGAGCTCA AGAGCGTCCG GATCCAAGCC CAGCCCTTCT CCAGAAAATA
AACATAGAAA CATTGTTACT CCCAGTTCAG AAATACTACT TTTGCCTAGA
ACTGTTTCTC TGAAAACCTGA GGGCCCTTAT GATTCTTAG ATTACATGAC
AACCACCAGA AAAATATATT CATCTTACCC TAAAGTCCAA GAGACACTTC
CAGTCACATA

TTAACCCACACA TCAGATGGGAA AAGAAATTAA GGATGATGTT GCCACAAATG
 TTGACAAACA TAAAAGTGAC ATTTTAGTCA CTGGTGAATC AATTACTAAT
 GCCATACCAA CTTCTCGCTC CTTGGTCTCC ACTATGGGAG AATTTAAGGA
 AGAATCCTCT CCTGTAGGCT TTCCAGGAAC TCCAACCTGG AATCCCTCAA
 GGACGGCCCA GCCTGGGAGG CTACAGACAG ACATACCTGT TACCACTTCT
 GGGGAAAATC TTACAGACCC TCCCCTTCTT AAAGAGCTTG AGGATGTGGA
 TTTCACTTCC GAGTTTTTGT CCTCTTTGAC AGTCTCCACA CCATTTCAAC
 AGGAAGAAGC TGGTTCTTCC ACAACTCTCT CAAGCATAAA AGTGGAGGTG
 GCTTCAAGTC AGGCAGAAAC CACCACCCTT GATCAAGATC ATCTTGAAAC
 CACTGTGGCT ATTCTCCTTT CTGAAACTAG ACCACAGAAT CACACCCCTA
 CTGCTGCCCC GATGAAGGAG CCAGCATCCT CGTCCCCATC CACAATTCTC
 ATGTCTTTGG GACAAACCAC CACCACTAAG CCAGCACTTC CCAGTCCAAG
 AATATCTCAA GCATCTAGAG ATTCCAAGGA AAATGTTTTT TTGAATTATG
 TGGGGAATCC AGAAACAGAA GCAACCCCGAG TCAACAATGA AGGAACACAG
 CATATGTCAG GGCCAAATGA ATTATCAACA CCCTCTTCCG ACCGGGATGC
 ATTTAACTTG TCTACAAAGC TGGAATTGGA AAAGCAAGTA TTTGGTAGTA
 GGAGTCTACC ACGTGGCCCA GATAGCCAAC GCCAGGATGG AAGAGTTCAT
 GCTTCTCATC AACTAACCAG AGTCCCTGCC AAACCCATCC TACCAACAGC
 AACAGTGAGG CTACCTGAAA TGTCCACACA AAGCGCTTCC AGATACTTTG
 TAACTTCCCA GTCACCTCGT CACTGGACCA ACAAACCGGA AATAACTACA
 TATCCTTCTG GGGCTTTGCC AGAGAACAAA CAGTTTACAA CTCCAAGATT
 ATCAAGTACA ACAATTCTCT TCCCATTGCA CATGTCCAAA CCCAGCATTC
 CTAGTAAGTT TACTGACCGA AGAACTGACC AATTCAATGG TTAATCCAAA
 GTGTTTGGA ATAACAACAT CCCTGAGGCA AGAAACCCAG TTGGAAAGCC
 TCCCAGTCCA AGAATTCCTC ATTATTCCAA TGGAAGACTC CCTTTCTTTA
 CCAACAAGAC TCTTTCTTTT CCACAGTTGG GAGTCACCCG GAGACCCCG
 ATACCCACTT CTCCTGCCCC AGTAATGAGA GAGAGAAAAG TTATTCCAGG
 TTCCTACAAC AGGATACATT CCCATAGCAC CTTCCATCTG GACTTTGGCC
 CTCCGGCACC TCCGTTGTTG CACACTCCGC AGACCACGGG ATCACCTCA
 ACTAACTTAC AGAATATCCC TATGGTCTCT TCCACCCAGA GTTCTATCTC
 CTTTATAACA TCTTCTGTCC AGTCCTCAGG AAGCTTCCAC CAGAGCAGCT
 CAAAGTTCTT TGCAGGAGGA CCTCCTGCAT CCAAATTCTG GTCTCTTGGG
 GAAAAGCCCC AAATCCTCAC CAAGTCCCCA CAGACTGTGT CCGTCACCGC
 TGAGACAGAC ACTGTGTTCC CCTGTGAGGC AACAGGAAAA CCAAAGCCTT
 TCGTACTTG GACAAAGGTT TCCACAGGAG CTCTTATGAC TCCGAATACC
 AGGATACAAC GGTTTGAGGT TCTCAAGAAC GGTACCTTAG TGATACGGAA
 GGTTCAAGTA CAAGATCGAG GCCAGTATAT GTGCACCGCC AGCAACCTGC
 ACGGCCTGGA CAGGATGGTG GTCTTGCTTT CGGTCACCGT GCAGCAACCT
 CAAATCCTAG CCTCCCCTA CCAGGACGTC ACTGTCTACC TGGGAGACAC
 CATTGCAATG GAGTGTCTGG CCAAAGGGAC CCCAGCCCCC CAAATTCCT
 GGATCTTCCC TGACAGGAGG GTGTGGCAAA CTGTGTCCCC

CGTGGAGAGAGC CGCATACACCC TGCACGAAAA CCGGACCCTT TCCATCAAGG
AGGCGTCCTT CTCAGACAGA GGCGTCTATA AGTGCGTGGC CAGCAATGCA
GCCGGGGCGG ACAGCCTGGC CATCCGCCTG CACGTGGCGG CACTGCCCCC
CGTTATCCAC CAGGAGAAGC TGGAGAACAT CTCGCTGCCC CCGGGGCTCA
GCATTCACAT TCACTGCACT GCCAAGGCTG CGCCCCCTGCC CAGCGTGCGC
TGGGTGCTCG GGGACGGTAC CCAGATCCGC CCCTCGCAGT TCCTCCACGG
GAACTTGTTT GTTTTCCCCA ACGGGACGCT CTACATCCGC AACCTCGCGC
CCAAGGACAG CGGGCGCTAT GAGTGCCTGG CCGCCAACCT GGTAGGCTCC
GCGCGCAGGA CGGTGCAGCT GAACGTGCAG CGTGCAGCAG CCAACGCGCG
CATCACGGGC ACCTCCCCGC GGAGGACGGA CGTCAGGTAC GGAGGAACCC
TCAAGCTGGA CTGCAGCGCC TCGGGGGACC CCTGGCCGCG CATCCTCTGG
AGGCTGCCGT CCAAGAGGAT GATCGACGCG CTCTTCAGTT TTGATAGCAG
AATCAAGGTG TTTGCCAATG GGACCCTGGT GGTGAAATCA GTGACGGACA
AAGATGCCGG AGATTACCTG TGCGTAGCTC GAAATAAGGT TGGTGATGAC
TACGTGGTGC TCAAAGTGGA TGTGGTGATG AAACCGGCCA AGATTGAACA
CAAGGAGGAG AACGACCACA AAGTCTTCTA CGGGGGTGAC CTGAAAGTGG
ACTGTGTGGC CACCGGGCTT CCCAATCCCG AGATCTCCTG GAGCCTCCCA
GACGGGAGTC TGGTGAAGTC CTTTCATGCAG TCGGATGACA GCGGTGGACG
CACCAAGCGC TATGTCGTCT TCAACAATGG GACACTCTAC TTTAACGAAG
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Human OCP: predicted amino acid sequence

MKVKGRGITC	LLVSFAVICL	VATPGGKACP	RRCACYMPTE	VHCTFRYLTS
IPDSIPPNVE	RINLGYNLSV	RLMETDFSGL	TKLELLMLHS	NGIHTIPDKT
FSDLQALQVL	KMSYNKVRKL	QKDTFYGLRS	LTRLHMDHNN	IEFINPEVFY
GLNFLRLVHL	EGNQLTKLHP	DTFVSLSYLQ	IFKISFIKFL	YLSDNFLTSL
PQEMVSYMPD	LDSLYLHGPN	WTCDCHLKWL	SDWIQEKPDV	IKCKKDRSPS
SAQQCPLCMN	PRTSKGKPLA	MVSAAAFQCA	KPTIDSSLKS	KSLTILEDSS
SAFISPOGFM	APFGSLTLNM	TDQSGNEANM	VCSIQKPSRT	SPIAFTEEND
YIVLNTSFST	FLVCNIDYGH	IQPVWQILAL	YSDSPLILER	SHLLSETPQL
YYKYKQVAPK	PEDIFTNIEA	DLRADPSWLM	QDQISLQLNR	TATTFSTLQI
QYSSDAQITL	PRAEMRPVKH	KWTMISRDN	TKLEHTVLVG	GTVGLNCPGQ
GDPTPHVDWL	LADGSKVRAP	YVSEDGRILI	DKSGKLELQM	ADSFDTGVYH
CISSNYDDAD	ILTYRITVVE	PLVEAYQENG	IHHTVFIGET	LDLPCHSTGI
PDASISWVIP	GNNVLYQSSR	DKKVLNNGTL	RILQVTPKDQ	GYRCVAANP
SGVDFLIFQV	SVKMKGQRPL	EHDGETEGSG	LDESNPIAHL	KEPPGAQLRT
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Year	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
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